

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number:121831

TO: Jon Ashen

Location: REM-2B02/2C18

Art Unit: 1635

Friday, May 14, 2004

Case Serial Number: 09/673994

From: Toby Port

Location: Biotech-Chem Library

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Ashen,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



model - nucleic search, using sw OM nucleic

Run on:

May 13, 2004, 10:04:10 ; Search time 1380 Seconds (without alignments) 11842.622 Million cell updates/sec

US-09-673-994A-7 3847 Title: Perfect score:

Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

3373863 segs, 2124099041 residues Searched: 6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N. Geneseq 290an04:*

1. geneseqn1980s:*
2. geneseqn2000s:*
4. geneseqn2001as:*
5. geneseqn2001bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

	Description	z35	Aaz35053 Mouse CNR	Aaz35052 Mouse CNR	_	Acc83474 Rat chond	Aba82987 Human tra	_	1 Human	Aai59942 Human pol	Aak85394 Human imm	Aal04937 Human rep	Ab197831 Human tes	Aba15877 Human ner	Ada53558 Human cod	Human		FIN13	Aaz35050 Mouse EST	Aax00648 Human sec	Aah97867 Murine 7-	Aaz35045 Mouse EST	G	Aah97866 Murine 7-	
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ALIGNMENTS

AAZ35044 standard; cDNA; 3847 BP Mouse CNREB-2 cDNA clone KND42. (first entry) 28-FEB-2000 AAZ35044; RESULT 1

CNREB-2; CNRE binding factor; transcription factor; mouse; renin; negative regulatory element; cardiovascular disease; hypertension; congestive heart failure; diagnosis; therapy; ss.

Mus musculus

Location/Qualifiers 1198. .3489 /*tag= a 3809. .3814 /*tag= b polyA_signal Key

WO9955343-A1.

04-NOV-1999

98US-0082997P. 99WO-US008502 24-APR-1998; 23-APR-1999;

(BGHM) BRIGHAM & WOMENS HOSPITAL INC.

Tamura Dzau VJ, Chen YE, Horiuchi M,

WPI; 2000-062002/05. P-PSDB; AAY32375.

A new regulatory element binding factor used to treat an adverse cardiovascular condition.

Claim 1; Page 77-79; 57pp; English.

This is the nucleotide sequence of cDNA clone KND42 encoding mouse negative regulatory element binding transcription factor CNREB-2. KND42 was obtained using yeast one-hybrid cloning and mouse kidney cDNA library screening. CNREB-2 binds to the 5' flanking region of the renin gene and

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modulates expression of the gene. 2 Other isoforms (see AAY32376-77) of CNREB-2 have been identified, the shortest isoform showing strongest binding activity to the CNRE of the renin promoter. CNREB-2 shares no significant homology to any other known gene or protein. It is a novel zinc finger transcription factor. Expression vectors, isolated mucleic acid molecules and CNREB-2 polypeptides are claimed, The invention also relates to CNREB-1 polymucleotides (see AAZ35040-43), polypeptides (see AAY32374) and inhibitors, and their use in claimed methods for decreasing expression, and for determining the level of CNREB-1 expression, and for determining the level of CNREB-1 expression, an increase in expression being indicative of an increase gusceptibility to development of a renin-angiotensin system mediated
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Sequence 3847 BP; 805 A; 1008 C; 1171 G; 852 T; 0 U; 11 Other;

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441	ACCTGAGCTGGATTCCGGGGCGGGGCGGGGCTGCCCAGGGCCCGCACC 15
501	GGGGGGGGTTCGTGGATCCTAAGAGCAAGGACCGACGGCGGAGGCCGAACTGGGA 15
501	GGGGGCGGTTCGTGGATCCTAAGAGCAAGGACCGACGGCAGGCCGAACTGGGA 1
19	GGGCCGGGAGCCTCGGGCCGCGAGGCGCGTCGGGCTTGGAGCCGGTCACGATGCC 1
561	EGGGGCCGGGAGGCCTCGGGCGGGGGGGGGGGGGGGGGGG
621	agaaggaaagccatccacagcccgtgaatgcgagggggggtcaaaggtca
681	TCAGGTCAGGGTG 1
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801	GGGTCAICGAGTACGGGAAGTGCAGTTCACAACAGCTGGCTCCTTG
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861	GCACCCTCCCCTCTTTAGTG 1
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     therapy;
                                                                                                                                                                                                                                                    Dzau VJ, Tamura K;
                                                                                                                                                                                                                            (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
     failure; diagnosis;
                                                 Location/Qualifiers 674. .2293 /*tag= a 2613. .2618 /*tag= b
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P-PSDB; AAY32377.
     congestive heart
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1437 1198 ATGGAGGGGCACAGGTACCACCTTCCTGGTTGGCTGGGTTGGGTTACGCGTCCAGCTTCTG 1257 1258 ATTGGTTGGCTAGCAGCGCATCACAATCACTTCCTGGTCATGCTGCGACTGCGCTCCGGT 1317 1377 GGCGGCGGGACCTGAGCTGGATTCCGGGGCCGGGG-CAGGGGCTGCCCAGGGCCCG 1496 180 120 9 1 ATGGAGGGGGCAGGGTACCACCTTCCTGGTTGGCTTGGGTTAGGGTTACGCGTCCAGCTTCTG ACGGAGGTACCAGCTGGTCTTCGGAGGGGGGGTAGGGGGCTCCATGAATGGAAGCGGCGGC TGTACAGCCCATGAACTACGCATCCCGTGTTGCTCTGCGGTGGCGGAAGCGGAAGCGGGT 1; Gaps ery Match 68.3%; Score 2628.4; DB 3; Length 2651; st Local Similarity 99.7%; Pred. No. 0; tches 2643; Conservative 0; Mismatches 7; Indels 1; 1318 1378 438 61 121 241

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2396 1200 2456 1616 1916 1976 2096 2156 2216 2276 1080 2336 1736 CTGTGGCTTTCGATGCTGTGCTCCACGACCAACCCGGCCTCCCAGTCCCACAGAGCAGGA 2636 GGTGGAGGGGACTCCTCAGGGTTAGGGGCGGATGATCTGGGATCTTCGCTCCTTACCAG 1796 540 720 780 900 960 GGGCAACCTGAGGGGGCATCAGCGCACCCACACAGGCCTCCCACTCCTCCTCCTCCTGCCCAAC GGTCAGGGGCCTTGAGCCGGGAGGAACAGGGGTGGGGTCAGTAGAGTGGGCTCAGGTCAG CAACGACCAGTCATGGGCTTTGAGAGAGTCTGAAGGAGACTCTCAGGGGGCCAGACC 961 GAGTGAAGTTGAGGAACCAGCCAGGGGTCCAGGGGAGGCCAGGGGTGAGAGGCCAGGCCC 1021 AGCCTGTCAGCTGTGTGGGGGGCCGACAGGTGAGGGGCCGTGTTGTGGGGGCAGGAGGG 1261 CACCCATACTGGCGAGAGCCCTACCGCTGTCCCCACACCCCTTTGCCTGCAGCAGCCT 2517 GGGCAACCTGAGGCGCCATCAGCGCACCCACACAGGGCCTCCCACTCCTCCCTGCCCAAC CTTGGTTCGGATTATGGTACTGCTTGGGAGGGAGAATTCCACAAAGCACCCCCCTCTTT AGIGGATACTGAAGATTCCTTCGACGAAGGTCCTGGGGGCCCTGGTGTTGGAGAGCGATTT GCTACTAGGCCAAGATCTGGAGTTTGAAGAGGAAAGAGGAGGAAGATGAAGGTGACGGCCA TOGACTICCCTATGGGCTGAGTGACGACGAGTCTGGGGGCGGCCGCGCACTAAGTGCGGA 901 IGGACTICCCTAIGGGCIGAGIGACGACGAGICIGGGGGGCGGCGCGCGCACIAAGIGCGGA 2157 GAGTGAAGTTGAGGAACCAGCCAGGGTCCAGGGGAGGCCCAGGGTGAGAGGCCAGGCCC CCGCTGTGGCCCCATACGCNTCAGCCCAGTTCGTCAACCTGACGCGACATACCCG CACCCATACTGGCGAGAAGCCCTACCGTTGTCCCCCACTGCCCTTTGCCTGCAGCCT GGGAGGGGGGGGCGGGGCCTCGGGCCGGAGGCGCGCGCTGGAGCCGGTCACGA TGCCCCGGAAGGAAAGCCATCCACAGCCCGTGAAATGCGAGGGGGGTCAAAGGTCAGG GGTCAGGGGCCTTGAGCCGGGAGGAACAGGGGTGGGTCAGTAGAGTGGGCTCAG AGTATTAAAGGAACCTGAGGTCATCGAGTACGGGAAGTGCAGTTCACAACAGCTGGCTC 2217 AGCCTGTCAGCTGTGGGGGGCCGACAGGTGAGGGGCCGTGTTGTGGGGCCAGGAGGCG 1081 GGGTGGGGGGCCCCCCCCCCCCCCCCCTTACTGTACTCATGCCGGCTGTGCGCTTTCGT 2397 2577 2277 2457 g d 셤 8 g 쉱 ò 셤 ò à δ ò

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This is the nucleotide sequence of a cDNA clone encoding mouse negative regulatory element binding transcription factor 2 (CNREB-2) short isoform CNREB-25. The clone was obtained using yeast one-hybrid cloning and mouse kinney CNNA library screening. CNREB-2 binds to the 5' flanking region of the remin gene and modulates expression of the gene. 2 Other isoforms (see AAY32375 and AAX32377) of CNREB-2 have been identified, the short of isoform showing strongest binding activity to the CNRE of the remin promoter. CNREB-2 shares no significant homology to any other known gene or protein. It is a novel zinc finger transcription factor. Expression or protein. It is a novel zinc finger transcription factor. Expression or protein. It is a novel zinc finger transcription factor. Expression claimed. The invention also relates to CNREB-1 polymorlectides (see AAX35040-43), polypeptides (see AAY32374) and inhibitors, and their use in claimed methods for decreasing or increasing remin expression, and for determining the level of CNREB-1 expression, an increase in expression and in any and increase in expression.
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The present sequence is that of a contig containing most of the murine Czf-1 coding sequence, lacking only the 5' portion which codes for the Neterinius of Czf-1 protein. The contig was obtained by screening mouse expressed sequence tag sequences using rat Czf-1 protein as a sequence probe. Czf-1 protein as a sequence probe. Czf-1 is expressed in a variety of tissue types, particularly of steoblasts and chondrocytes. It is expressed in the nuclei of hypertrophic chondrocytes of the growth plate, and exhibits an alternate expression and intracellular localisation pattern in cells expressing high, i.e. constitutively active, levels of fibroblast growth factor receptor (FGGR). It is up-regulaced in osteoarthritic cartilage tissue and serves as a marker for osteoarthritis. Czf-1 has been found in rats, mice and humans. Sequence identity for nuclectide and amino acid sequences is above 85%. Czf-1 polynuclectides, polypeptides and serves as the characterisation, diagnosis and treatment of FGRR-related and skeletal diseases and disorders, such as osteoarthritis, rheumatoid arthritis, and cartilage related diseases
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                                                                                               New chondrocyte-derived zinc finger polypeptides and encoding polynucleotides, useful for detecting, diagnosing and treating C protein-related diseases, such as osteoarthritis and rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse chondrocyte-derived zinc finger protein Czf-1 partial cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Mouse Czf-1"
/note= "No start codon"
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3. .1355
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The present sequence is that of cDNA was isolated from a glioma CDNA protein, designated Czf-1. The cDNA was isolated from a glioma cDNA library using a probe from the 3' end of the Czf-1 gene. Czf-1 is expressed in a variety of tissue types, particularly osteoblasts and chondrocytes. It is expressed in the nuclei of hypertrophic chondrocytes of the growth plate, and exhibits an alternate expression and intracellular localisation pattern in cells expression and constitutively active, levels of fibroblast growth factor receptor (FGFR). It is up-regulated in osteoarthritic cartilage tissue and serves as a marker for osteoarthritis. Czf-1 has been found in rats, mice and humans. Sequence identity for nucleotide and anino acid sequences is above 85%. Czf-1 polymucleotides, polypeptides and antibodies can be used in the characterisation, diagnosis and treatment of FGFR-related and skeletal diseases and disorders, such as osteoarthritis, rheumatoid arthritis, and cartilage related diseases
1621 AACTGGTTGGGAGCTGCCCAGCCTTTTACTGTTTTAACTTATTTCAGTGCTTTATAATAA 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1917 AGTGGATACTGAAGATTCCTTCGACGAAGGTCCTGGGGGCCCTGGTGTTGGAGGGATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New chondrocyte-derived zinc finger polypeptides and encoding polymucleotides, useful for detecting, diagnosing and treating of protein-related diseases, such as osteoarthritis and rheumatoid arthritis.
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                               3814 AGGAAACACTAACAGA 3829
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229 AGTGGATACTGAAGATTCCTTCGACGAAGACTCTGGGGGCTCTGGTGTTGGAAGATGTTT 288 289 GCTACTAGGCCAAGATTCGAAGATTCGAAGAAGAGAAGA	GGGGAACCTGAGGGGAAGCCCTACCGCCTGCCCCTTTGCTGCTGCTGCCCAC GAGCCAAACTGGGGGAATCAGGGCACCCACACTGCCCCCTTTGCTGCCCCAC GGGGCAACCTGAGGGCATCAGGGCACCCACACTGCCCCCTTTGCTGCCCCAC GGGCAACCTGAGGGCATCAGGGCACCCACACGGCCTCCCACTCCTCCTGCCCCAC GGGCAACCTGAGGCGCATCAGGCGCACCCACACGGCCTCCCACTCCTCCTGCCCCAC CTGTGGTTTCCGATGCTGTGCTCCACGACCCACCCGGCCTCCCACTCCTCCTGCCCCAC CTGTGGTTTCCGATGCTGTGCTCCACGACCCACCCGGCCTCCCAGAGCAGA GGGGACAATGCCCCGACACACACCACCCACCCGGCCTCCCAGAGCAGA GGGGACAATGCCCCGACACACACACCACCCGGCCTCCCAGACCTGGATCTCATGT GGCACCAGGGGACCCAGAACACCACCCACACCCGGCCTGGACCTGGATCTCATGT GCCACCAGGGTGCCCCAGAACACCACCACCAGAGCTGGACTTCCTTGGACCTGGTGTGT GCCACCAGGGTGCCCAGATTTCTTCTGCCAGAGCTGGACTTCTTGGACCTGGTGGGGA GCCACCAGGGTGCCACACCACCACCACGAGCTGGACTGGACCTGGTGTGTGGGCG CTGTGGTGGAACTGGAACCACCACCACGAGCTGCCAGGGGGGGG
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AGACTCACCTTGAACTAACTAGTTCTTTTACCTGGGGCTCTAGGAATTAGCCCTATGCC 3536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, transcription factor, TRFX, cell proliferative disease, autoimmune disease, inflammation, neurological disease, developmental disorder; cancer, AIDS, infection, cytostatic, anti-HIV, neuroprotective, antiinflammatory, gene therapy, ds.
                                                                                                                                                                                                                                       AGCAGGAGGCCTGGTCTCTGGCCCTGAGGCTGGGCCCCACCTCATAGCCCACCTC
                                                                                                                                                                                                                                                                                                  CCCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAACGTCAAGGTCGCATCCA
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                                                                                                          CCTCAAACGTCATATGCTGCGACACACGGGCGAGAAGCCCTTCCGCTGTGCCCTGCGC
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3057 TCATCTGGATAACCTGAAACGGCACCAGGCGCGTCCACACAGGAAAAGCCCTACAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel transcription factor polypeptides, used to treat diseases
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Tang YT, Mathur P, Shah P, Au-Young
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TCCTGCATTTTATAC 1860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA82987 standard; DNA; 1975
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Azimzai Y, Bandman O,
Reddy R;
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P-PSDB; ABB50163.
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2637 GGGGACAATGCCCCGACGATGAGAAATGCGCTGATCCTGCCAGACTTGAGTCTTCATGT 2696

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pr associated with altered activity and expression of TRFX, and to screen XX
PS Claim 11; Page 261; 327pp; English.

CC dator. The present sequence is the coding sequence for a human transcription factor and its coding sequence are useful in the present sequence is the coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with the diagnosis, treatment and prevention of diseases associated with the diagnosis, treatment and prevention of diseases associated with a the diagnosis, treatment and prevention factor e.g. cell proliferative, curoimmune/inflammatcry, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification, comparing arteriosclerosis, cirrhosis, hepatitis, concert, and action asthma, autoimmune thyroiditis, bronchitis, atopic dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, confers, cisease, multiple sclerosis, osteoarthritis, pancreatitis, conficis, uveitis, diabetes mellitus, disease, Huntington's disease, parkinson's disease, stroke, and viral, bacterial, fungal and protozoal infections XX
Coguence 1975 BP; 396 A; 625 C; 612 G; 342 T; 0 U; 0 Other;
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2456 2096 2156 2216 2276 2336 2396 CACCCATACTGGCGAGAAGCCCTACCGTTGTCCCCACTGCCCCTTTGCCTGCAGCAGCCT 2516 GGGCAACCTGAGGCGCATCAGCGCACCCACACAGGGCCTCCCACTCCTGCCCAAC 2576 CTGTGGCTTTCGATGCTGTGCTCCACGACCAACCCGGCCTCCCAGTCCCACAGGAGGAGGA 2636 2036 385 685 205 325 CTGTGGCTTCCGCTGCTGTACTCCACGACCAGCCCGGCCTCCCAGACTCCACAGAGCAGGA 805 1917 AGTGGATACTGAAGATTCCTTCGACGAAGGTCCTGGGGCCCTGGTGTTGGAGAGCGATTT TGGACTTCCCTATGGGCTGAGTGACGACGAGTCTGGGGGCGCCCCCGCCACTAAGTGCGGA 266 TGGGCTTCCCTATGGGCTGAGCGACGATGTGAGTCTGGGGGCGGCCGGGCACTAAGTGCGGA GAGTGAAGTTGAGGAACCAGGCAGGGTCCAGGGGAGGCCAGGGGTGAGAGGCCAGGCCC 326 GAGTGAAGTTGAGGAGCCAGCCAGGGGTCCAGGGGAGGCCAGGGGTGAGAGGCCAGGGCC AGCCTGTCAGCTGTGTGGGGGGCCCGACAGGTGAGGGGCCGTGTTGTGGGGGCAGGAGGGCG AGCCTGCCAGCTGTGTGGGGGGGGCGACAGGTGAGGGCCCTGCTGTTGTGTGGGGCCAGGAGGCC CCGCTGTGGCCGCTGCCCATACGCNTCAGCCCAGTTCGTCAACCTGACGCGACATACCCG GGGCAACCTGAGGCGGCATCAGCGTACCCACGCAGGGCCCCCCCACTCCTCCTGCCCGAC 86 AGTGGATACTGAAGACTCCCTCGAGGACCCCCGGGGCCCTGGTATTGGAGAGTGATTT GCTACTAGGCCAAGATCTGGAGTTTGAAGAGGAAGAAGAGGAAGAGGATGAAGGTGACGGCCA 2037 CAACGACCAGCTCATGGGCTTTGAGAGAGACTCTGAAAGAAGACTCTCAGGGGGCCAGACC 206 CAGTGACCAGCTCATGGGCTTCGAGAGACTCGGAAGGAGACTCTCTGGGGGCCCAGGCC GGGTGGGGGCCCCCCCCCCCCCCCCCCCCCTGTACTCATGCCGGCTGTGCGCCTTTCGT 446 degradadadaccentacracececenacianacraraceaecereracarecraraceae Query Match 38.9%; Score 1498; DB 5; Length 1975; Best Local Similarity 88.6%; Pred. No. 0; Matches 1707; Conservative 0; Mismatches 176; Indels 44; Gaps 386 999 626 2517 989 2097 2217 2277 2337 2457 2577 2157 2397 1977

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DP	908	GGGGGCGGTGCCCCGGCGACCTGAAGATGCTCTTCCTTTCCAGATTTGAGCCTCCATGT 865
δλ	2697 (GCCACCAGGTGGTGCCAGTTTCCTGCCAGACTGTGGGCAGCTGCGGGGGTGAAGGGGAGAG 2756
QQ	866 (SCCACCAGGTGCCAGTTTCCTGCCAGACTGTGGGCAGCTGTGTGTG
δ	2757 (CTIGIGIGGAACIGGAICCGAACCACIGCCAGAGCIACIGTICCCTIGGACCIGCCGGGG 2816
дg	926	crecesearcesarcasaaccacasascrecrarrecraresascreces
ò	2817	CTGTGGACAGGAACTGGAGGAGGCAGCAGGCAGGCAGGGAGCTGCGATGTGGGGG 2876
qq	986	crórigakchadacrigakdadadarakdrodacrigadakorigocardrodada 1045
ò	2877	CTGCATGCGAGGAGGAGGAGGAGGGGAGCACTGGGGGGAGCCCCAGGGCCCTGGTGACAA 2936
qq	1046	cticiandicaaddaddectidaadddaddaddadddaddadadadaa 1105
δ	2937	AGGCTITGCCTGTAGTITTATGCCCCTTTGCCACTCACTACCCCCAACCACCTGGCTCGGCA 2996
QC QC	1106	-11
٥x	2997	CATGAAGACTCACAGTGAGAAAACCCTTCCGCTGTGCCCGCTGTCCATACGCCTCTGC 3056
Dþ	1166	saadacacacacadadadadacccrrccecrdceccccccccrcrrareccrcrcra
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ପ୍ର	1226	carcresaraaccreaaacecaceae
٥'n	3117	CCCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAAGCGTCATGGTCGCATCCA 3176
ΩÞ	1286	TCTGCCCTTATGCCTGTGGCAATCTGGCCAACCTCAAGCGTCATGGTC
δ	3177	CTCTGGTGACAAACCTTTTCGGTGTAGCCTTTGCAACTACAGCTGCAACCAGAGTATGAA 3236
qq	1346	crendarchalacerrinedargraecerrechaetacagergearceagacargaa 1405
&	3237	29
Op	1406	cerchancercachrecrecachchchadecearthcearchdechacachcedec
8	3297	CTATACCACAGGCCACTGGGACAACTACAAGCGTCATCAGAAGGTGCATGGCCATGGTGG 3356
qq	1466	CTATACCACGGGCCACTGGGGACAACTACAAGGGCCACCAGAAGGTGCTTTTTTTT
δ	3357	AGCAGGAGGCCTGGTCTCTGCCCCTGAGGGTGGGCCCCACCTCATAGCCCACCTC 3416
οp	1526	THE STATE OF THE S
ò	3417	TGTTTTGAGCACTCGGGGTCCAGCAGCCCTGGGGACTACTAGGTAGCAGGGCTCTTCATTC 3476
q 0	1586	iditiilaaciicicaaaccaaccaacciaaaaciaciaacaacaac
ò	3477	AGACTCACCTIGAACIAACTAGGTICTITIACCIGGGGCTCTAGGAATTAGCCCTAIGCC 3536
ΩÞ	1646	AGACTCATCCTGAACTAGGTCCTTCTT 1672
δ	3537	TCTGCATTITATACAAATGAAACTAGAAACCACTTTCCCTTTCTCCCCGCTGGTCAGG 3596
d d	1673	-TTTCTCCCCCCCTGCCAG
ò	3597	GGCTCCACACAGACTAACCTAGGCACTATATGGACCAGCTGAATCCCATGGTCAGGGGG 3656
QQ	1729	CTCCACA
ò	3657	-CCATATAGACCAGGGA-CITGICITAGCICACGTACCAGAIGAGCTAAGTGATTAGGG 3714
дg	1789	cccatatiggaccadedectrocctroactgacdcacrrcacgagcrcagrgaggaggg 1848
ò	3715	CCTIGGATICACCGCCACIGCICCCAGAGGCIAIGGAIGAACTGGIIGGGAG-CIGCCCA 3773

The present sequence is that of CDNA encoding a novel human zinc finger protein, designated Czf-1. Czf-1 is expressed in a variety of tissue nuclei, designated Czf-1. Czf-1 is expressed in a variety of tissue nuclei by particularly offerbolasts and chondrocytes. It is expressed in the nuclei of hypertrophic chondrocytes of the growth plate, and exhibits an alternate expression and intracellular localisation pattern in cells factor receptor (FGFR). It is up-regulated in osteoarthritic cartilage tissue and serves as a marker for osteoarthritis. Czf-1 has been found in rats, mice and humans. Sequence identity for nucleotide and amino acid sequences is above 85%. The human gene maps to chromosome 2p22-23. Czf-1 polynucleotides, polypeptides and antibodies can be used in the disarcters acid in disponsels and treatment of FGFR-related and skeletal diseases and disorders, such as osteoarthritis, rheumatoid arthritis, and cartilage related diseases CCTGTATTCACCTCCACTGCCCCCAGGGGCTGTGGACAAACCGGCTGGGGGACTGCCCA 1908 1909 GCCTCCCACCTGTTATTTAACTTATTTTCAGTGCTTTATAATAAAGGAAACACTAACAAA 1968 GCCTTTTAC----TGTTTTAACTTATTTCAGTGCTTTATAATAAAGGAAACACTAAACAGA Czf-1 Human, Czf-1, chondrocyte; zinc finger; osteopathic; antiarthritic; antirheumatic; chromosome 2p22-23; gene; ss. New chondrocyte-derived zinc finger polypeptides and encoding polymucleotides, useful for detecting, diagnosing and treating (protein-related diseases, such as osteoarthritis and rheumatoid arthritis. Sequence 1855 BP; 344 A; 590 C; 619 G; 302 T; 0 U; 0 Other; Human chondrocyte-derived zinc finger protein Czf-1 cDNA /product= "Human Czf-1" Location/Qualifiers 171. .1796 /*tag= a ACC83473 standard; cDNA; 1855 BP. rayon A, Blumenstein S, Harari Claim 12; Fig 1; 64pp; English. 20-NOV-2002; 2002WO-IL000925 20-NOV-2001; 2001US-0331626P (PROC-) PROCHON BIOTECH LTD (first entry) 3830 AAAAAA 3836 1969 AAAAAA 1975 WPI; 2003-457599/43. P-PSDB; ABR42912. WO2003044159-A2 Homo sapiens 08-SEP-2003 30-MAY-2003 3774 1849 RESULT 7 ACC83473 셤 ò ò

DB 7; Length 1855;

1392; No. 0;

Score Pred.

36.2%; 92.6%;

Query Match Best Local Similarity

2816 2876 1303 1123 2756 1063 2036 2096 2156 2216 2276 2336 2396 2456 2516 2576 2636 2696 1003 ö 643 703 823 883 943 523 403 463 1004 GCCACCAGGTGGTGCCAGTTTCCTGCCAGACTGTGGGCAGCTGCGGGGTGAAGGGGAGGG CTGCATGCGAGGAGGAGGCTGGAGGGGGGCGCAGGGGGGCCCCAGGGCCCCAGTGACAA 1244 AGGCTTTGCCTGTAGCCTCTGCCCCTTTGCCACTCACTATCCCAACCACCAGGCAGCA 944 GGGGGGGGGCGCGGGGGACCTGAAGATGCTCTCCTTCCAGATTGAGCCTCCATGT CTCTGCGGGACTGGATCAGAACCACTGCCAGAGCTGCTATTCCCTTGGACCTGCCGGG CIGIGACAAGAGCIGGAGGAGGGGAGGGAAGCIAGGAAGCIGCCAIGIGGAGGCG AGGCTTTGCCTGTAGTTTATGCCCCTTTGCCACTCACTACCCCCAACCACCTGGCTCGGCA CCGCTGTGGCCGCTGCCCATACGCNTCAGCCCAGTTCGTCAACCTGACGCGACATACCCG CACCCATACTGGCGAGAAGCCCTACCGTTGTCCCCCACTGCCCCTTTGCCTGCAGCAGCCT GGGCAACCTGAGGCGCATCAGCGCACCCACACAGGGCCTCCCACTCCTCCTGCCCAAC CTGTGGCTTCCGCTGCTGTACTCCACGACCAGCCCGGCCTCCCAGACTCCCACAGAGCAGGA GCCACCAGGTGGCCAGTTTCCTGCCAGACTGTGGGCAGCTGCGGGGTGAAGGGGAAGA CITGIGIGGAACTGGGAACCACTGCCAGAGCTACTGTTCCCTTGGACCTGCCGGGG CTGTGGACAGGAACTGGAGGAGGTGAGGCAGCAGGTGGGAGCTGCCATGTGTGGGGC CTGCATGCGAGGAGGCTGGAGGGTTGCCACTGGGGGACCCCCAGGGCCCTGGTGACAA 14 CAGTGACCCAGCTCATGGGCTTCGAGAGAGACTCGGAAGGAGACTCTCTGGGGGCCAGGCC 2217 AGCCTGTCAGCTGTGTGGGGGCCGACAGGTGAGGGGCCGTGTTGTGGGGGCAGGAGGGCG 524 Agccracchactraragagagaccaachagrahagagagacatararagagachagagacc CIGIGGCTITICGAIGCTGICCACGACCAACCCGGCCTCCCAGACTCCACAGAGCAGGA GGGGACAATGCCCCGACGATCAGAAAATGCGCTGATCCTGCCAGACTTGAGTCTTCATGT 1977 GCTACTAGGCCAAGATCTGGAGTTTGAAGAGGAAGAGGAAGAGGATGAAGGTGACGGCCA 2097 IGGACITICCCIATGGGCTGAGTGACGACGAGTCTGGGGGGCGGCCGCGCACTAAGTGCGGA geangagacccccaracccraagarracraracraaracraacaccacraracrar 584 egenegegececenecnecececececenecnecnes establicado es es es establicados establi 1917 AGTGGATACTGAAGATTCCTTCGACGAAGGTCCTGGGGCCCTGGTGTTGGAGAGGCGATTT 224 AGTGGATACTGAAGACTCCCTCGACGAAGGACCCGGGGGCCCTGGTATTGGAGAGTGATTT CAACGACCAGCTCATGGGCTTTGAGAGAGACTCTGAAGGAGACTCTCAGGGGGCCCAGAACC 2157 GAGTGAAGTTGAGGAACCAGGGGTCCAGGGGAGGCCAGGGGTGAGAGGCCAGGGCC Gaps .; 0 0; Mismatches 116; Indels Matches 1461; Conservative 704 2577 884 2757 1064 2817 1124 2877 1184 2037 464 2277 2337 2397 2457 764 2517 2637 2697 644 824 셤 Š g g ઠે g ð ద 8 a 셤 Ωp ò 셤 δ g 8 셤 ઠે Š 쉱 g d ð qq à 유 ઠે 8 쉱 ò ò ò 셤 à

1423 3416 TGTTTTGAGCACTCGGGGTCCAGCAGCCCTGGGTACTAGTAGCAGGCTCTTCATTC 3476 Human, secreted protein, cytokine, cell proliferation, nutritional supplement; immune modulation, autoimmune disorder; haematopoiesis regulation; tissue growth; haemostasis; inflammation; ss. CCCCTCTGCCCTTATGCCTGTGGCAATCTGGCCAACCTCAAGCGTCATGGTCGCATCCA CTATACCACAGGCCACTGGGACAACTACAAGCGTCATCAGAAGGTGCATGGCCATGGTGG **CATGAAGACTCACAGTGGTGAGAAACCCTTCCGCTGTGCCCGCTGTCCATACGCCTCTGC** CATGAAGACACACAGTGGTGGAAGAAGCCTTTCCGCTGCGCCCGCTGTCCTTATGCCTCTGC rcarcregaraaccregaaceecaccaecerccaracaegaagaagcccracaagre CCCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAACCTCAAGCGTCATGGTCGCATCCA CTCTGGTGACAAACCTTTTCGGTGTAGCCTTTGCAACTACAGCTGCAACCAGAGTATGAA CCTCAAACGTCATATGCTGCGACACACGGGCGAGAAGCCCTTCCGCTGTGCCACCTGCGC TCATCTGGATAACCTGAAACGGCACCAGGGGGTCCACACAGAGAAAAAGCCCTACAAGTG Human secreted protein coding sequence SEQ ID NO: 61. Location/Qualifiers
177. .1625
/*tag= a
/*tag= a
/*tag= b
/*tag= b
/*tag= b
/note= "potential signal peptide"
/*tag= e
/*tag= e
/note= "potential signal peptide" *tag= f note= "potential mature peptide" peptide /*tag= c /note= "potential mature 225. .1622 AGACTCACCTTGAACTA 3493 AGACTCATCCTGAACTA 1800 AAA93131 standard; cDNA; 1996 1622 (first entry) /*tag= WO200049134-A1 Homo sapiens 12-JAN-2001 mat_peptide sig_peptide sig_peptide mat_peptide 3477 3417 1724 1784 1304 3057 1364 3117 3177 3237 1544 3297 1604 3357 1664 AAA93131; 1424 1484 2997 RESULT 8 AAA9313 g 8 8 8 8 8 쉽 ò 8 8 8 8 g Š 셤 ઠે d

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the coding sequence for a human secreted protein. The sequence was isolated from an adult lung cDNA library. The proteins and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have tases as nutritional supplements, as cytokine or cell proliferation autoimmune diseases, as haematopoiesis regulators (treating mysloid or autoimmune diseases, as haematopoiesis regulators (treating mysloid or hymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438
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                                                                                                                                                                                                                                                                                                                                                     New secreted proteins and polynucleotides encoding them, which are derived from Homosapiens, useful for therapy, diagnosis, and research, well as nutritional sources or supplements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 GICCAGGGCAAGGCTGAGAGGCCAGGCCAGGCTGCCAGCTGTGTGGGGGGCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1996 BP; 449 A; 605 C; 578 G; 364 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 70; Page 288-289; 309pp; English
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(ALPH-) ALPHAGENE INC

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Goodrich R, Drmanac RT;
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, Zhao C
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                                                                                                                                                                                                                                                                                                                                             TATAAGGACCAGCCAACCCCATGGGCGGGGGCCCATATGGACCAGGGGACCTTGCCT
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encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous to localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhian activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemids and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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Sequence 1488 BP; 287 A; 460 C; 484 G; 257 T; 0 U; 0 Other;

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cch 1100 55; 20; 3; 100 C; 101 C; 20; 2; 20; 20; 20; 20; 20; 20; 20; 20;	al Similarity 92.9%; Fred. No. 4.1e-301; 1272; Conservative 0; Mismatches 97; Indels 0;	1885 GAGGGAGATTCCACAAGCACCTCCCTCTTTAGTGGATACTGAAGATTCCTTCGACGAA	1945 GGTCCTGGGGCCCTGGTTGGTTGGGATTTGCTACTAGGCCAAGATCTGGAGTTTGAA		2005 GAGGAAGAGGAGGATGAAGGTGACGGCCACAACGACCAGCTCATGGGCTTTGAGAGA	239 GAGGAAGAAGAAGAAGAAGAAGACGACGGCAACAGTGACCAGCTCATGGGCTTCGAGAA	65	299 GACTCGGAAGGAGTCTCTGGGGGCCAGGCCTGGGGCTTCCCTATGGGCTGAGGACGACGAT	2125 GAGTCTGGGGGCGGCGCACTAAGTGCGGAGAGAGAGAGGGAACCAGCCAG	359 GAGTUTGGGGGGCGGGCGCGGGCACTAAGTGCGGAGAGTGAAGTTGAGGAGCCAGCC	2185 CCAGGGGGGCCAGGCCAGCCCAGCCCTGTCAGCTGGGGGGCCGACCA	419 CCAGGGAGGCCAGGGGTGAGAGGCCCAGGCCCAGCCTGCCAGCTGTGTGTG	2245 GGTGAGGGCCGTGTTGTGGGGGGGGGGGGGGGGGGGGGCCCCCCC	479 GGTGAGGGCCGTGTTGTGGGGGCAGGGCCGGGTGGGGGCCCCCTGCTGCCTGC	2305 TTACTGTACTCATGCCGGCTGTGCGCTTTCGTGTCCCACTACTCGAGCCACCTGAAGCGG	539 CTACTGTACTCATGCCGCCTCTGCACCTTCGTGTCCCACTACTCGAGCCACCTGAAGCGG	2365 CACATGCAGACACACAGGGGGGAGAAGCCGTTCCGCTGTGGCCGCTGCCCATACGCNTCA	599 CACATGCAGACACACAGAGAGAGAGAGCGTTCCGCTGTGGCCGCTGCCCTACGCCTCA	2425 GCCCAGTTCGTCAACCTGACGCACATACCCGCACCCATACTGGCGGAGAAGCCCTACCGT	659 GCCCAGCTCGTCAACCTGACACACACACGCACCCACACTGGCGAGAAGCCCTACCGC	2485 IGTCCCCACTGCCCCTTTGCCTGCAGCAGCCTGGGCAACCTGAGGGGCATCAGGGCACC	719 TGTCCCCACTGCCCCTTTGCCTGCAGCCTGGGCAACCTGAGGCGGCATCAGCGTACC	2545 CACACAGGCCTCCCACTCCTCCCAACCTGTGGCTTTCGATGCTGTGCTCCACGA	779 CACGCAGGGCCCCCCCACTCCTCCTGCCCGACCTGTGCTTCCGCTGCTGTACTCCACGA	2605 CCAACCCGGCCTCCCAGTCCCACAGGGGGGGGGGACAATGCCCCGACGACGATCAGAAAT	839 CCAGCCCGGCCTCCCACCACACAGCAGGAGGGGGGGGGG	
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\$ a	3085 CGCGTCCACACAGAGAAAAGCCCTACAAGTGCCCCCTCTGTCCGTATGCCTGTGGCAAC 3144
ठ व	3145 CTGGCCAACCTCAAGGGTCATGGTCGCATCCACTCTGGTGACAAACCTTTTGGGTGTAGC 3204
& g	3205 CTTTGCAACTACAGCTGCAACAGAATATGAACCTCAAAGGTCATATGC 3253
RESI AAK ID XX XX	ULT 10 BS394 AAK85394 standard; DNA; 9266 BP. AAK85394;
X E X	07-NOV-2001 (first entry)
Z X X E	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40206. Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
X 8 X	Homo sapiens.
Z X 23	WO200157182-A2. 09-AUG-2001.
¥ # ¥	17-JAN-2001; 2001WO-US001354.
1 K K K K K K K K K K	31-JAN-2000; 2000US-0179065P. 24-FEB-2000; 2000US-0186628P. 24-FEB-2000; 2000US-018664P. 16-MAR-2000; 2000US-018874P. 17-MAR-2000; 2000US-019874P. 18-APR-2000; 2000US-019812P.
PR PR	28-JUN-2000; 2000US-0214886 30-JUN-2000; 2000US-0215135

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2000US-0249209P.
2000US-0249218P.
2000US-025039P.
2000US-0251989P. SCI INC Barash SC, (HUMA-) HUMAN GENOME WPI; 2001-483426/52 20-0CT-2000; 20-0C 05-JAN-2001; Rosen CA,

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 40206; 3071pp + Sequence Listing; English

AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I)

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polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87649 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM8169 represent sequences used in the exemplification of the present invention
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                                                                                                    Sequence 9266 BP; 2324 A; 2431 C; 2502 G; 2009 T; 0 U; 0 Other;
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31.1%; Score 1195; DB 4; Length 9266;
Best Local Similarity 81.3%; Pred. No. 2.9e-294;
Matches 1568; Conservative 0; Mismatches 216; Indels 144;
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14-SEP-2000; 2000US-0231368P.
14-SEP-2000; 2000US-0231368P.
14-SEP-2000; 2000US-023239P.
14-SEP-2000; 2000US-023239P.
14-SEP-2000; 2000US-023239P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-023400P.
14-SEP-2000; 2000US-023402P.
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21-SEP-2000; 2000US-023499P.
22-SEP-2000; 2000US-023499P.
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25-SEP-2000; 2000US-02344617P.
26-OCT-2000; 2000US-02346478P.
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26-OCT-2000; 2000US-02346478P.
26-OCT-2000; 2000US-02346478P.
26-OCT-2000; 2000US-02346478P.
26-OCT-2000; 2000US-02346478P.
26-OCT-2000; 2000US-02346528P.
26-NOV-2000; 2000US-02346528P.
26-NOV-2000; 2000US-02346528P.
27-NOV-2000; 2000US-02346528P.
     Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                                                               Human reproductive system related antigen DNA SEQ ID NO: 7625
                                                                       AAL04937 standard; DNA; 9266 BP
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2000US-018643BP.
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31.1%; Score 1195; DB 4; Length 9266;
Best Local Similarity 81.3%; Pred. No. 2.9e-294;
Matches 1568; Conservative 0; Mismatches 216; Indels 144;
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                                                                                                                                                                                                                                                                                                            inucleic acid molecule encoding a reproductive preventing, treating or ameliorating a medical
                                                                                                                                                                                                                                                   Ruben SM;
01-DEC-2000; 2000US-0250160P.

01-DEC-2000; 2000US-0250391P.

05-DEC-2000; 2000US-0251988P.

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06-DEC-2000; 2000US-025198P.

08-DEC-2000; 2000US-0251856P.

08-DEC-2000; 2000US-0251868P.

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3078 TGGCCAGGGGCTCCACACACAGACTAACGTAGGCACATAAAGGACCAGCCCAAGGG 3137
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2000US-0189374P.
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2000US-0214868P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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31.1%; Score 1195; DB 4; Length 9266;
Best Local Similarity 81.3%; Pred. No. 2.9e-294;
Matches 1568; Conservative 0; Mismatches 216; Indels 144; Gaps
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11-MAR-2000; 2
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20-UIN-2000; 2
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Human nervous system related polynucleotide SEQ ID NO 8208.

23-JAN-2002 (first entry)

ABA15877;

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkingonian; antisickling; antianemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antialiabetic; antillacr; anticonvulsant; antifungal; antiparastic; cardiate; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

Homo sapiens

WO200159063-A2.

16-AUG-2001.

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29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237037P.
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02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237039P.
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02-OCT-2000; 2000US-024647P.
03-NOV-2000; 2000US-024647P.
03-NOV-2000; 2000US-024647P.
03-NOV-2000; 2000US-024652P.
03-NOV-2000; 2000US-02492P.
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01-DEC-2000; 2000US-0251160P.

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08-DEC-2000; 2000US-0251868P.

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08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251868P.
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2000US-0250391P.
2000US-0251160P.
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ΩS (HUMA-) HUMAN GENOME SCI INC. Rosen CA, Barash SC,

WPI; 2001-541565/60

7227

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant) agonists are useful in the mucleic acids, proteins, antibodies and (ant) agonists are useful in the mucleic acids, proteins, antibodies and (ant) agonists are useful in the mucleic acids, proteins, antibodies and (ant) agonists are useful in breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune to search actions antibodies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders eugh arthritis and ulcerative colitis; (c) cardiovascular disorders eugh as wiral, bacterial, fungal and parsaitic infections Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly the multiple to multiple sclerosis, tral, bacterial is electronic format directly the multiple to multiple sclerosis intentions who was obtained in electronic format directly the multiple to multiple sclerosis and parsaitic. Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases. Disclosure; SEQ ID NO 8208; 1701pp + Sequence Listing; English.

Sequence 9266 BP; 2009 A; 2502 C; 2431 G; 2324 T; 0 U; 0 Other;

2542 2602 7528 2422 7408 2482 7587 2302 2063 GAGACTCTGAAGGAGACTCTCAGGGGGCCAGACCTGGACTTCCCTATGGGCTGAGTGACG
7166 CTATTTCACCAGGAGACTCTCTGGGGGCCAGGCCTGGGCTTGGCTTGCCTATGGGCTGAGCGACG CAGCCCAGTTCGTCAAACCTGACGCGACATACCCGCACCCATACTGGCGAGAAAGCCCTACC CCCACACAGGGCCTCCCACTCCTGCCCAACCTGTGGCTTTCGATGCTGTGCTCCAC CCCACGCAGGGCCCCCCCACTCCCTGCCCGACCTGTGGCTTCCGCTGCTGTTCTACTCCAC 2003 AAGAGGAAGAGGAAGAGATGAAGGTGACGGCCACAACGACCAGCTCATGGGCTTTGAGA 7826 AAGTGAAAAGGGGAGAGTTTGGAGCCTGATCCTACCTATGCTGATGTCTCTTTTATGT 7706 AIGAGTCTGGGGGCGGGGCCGGGCATTAAGTGCGGAGAGTGAAGTTGAAGTTGAGGAGCCAGGG CAGGTGAGGGGCCGTGTTGTGGGGCAGGGGGGGGGGGGCCCCCGCTGCCCCCAC GGTTACTGTACTCATGCCGGCTGTGCGCTTTCGTGTCCCACTACTCGAGCCACTGAAGC 2363 GGCACATGCAGACACACGGGGAGAAGCCGTTCCGCTGTGGCCGCTGCCCATACGCNT GITGICCCCACTGCCCCTTTGCCTGCAGCCTGGGCAACCTGAGGGGGCATCAGCGCA 2123 ACGAGTCTGGGGGGGGGCGCCACTAAGTGCGGAGAGTGAAGTTGAGGAACCAGGG GACCAACCCGGCCTCCCAGTCCCAGAGGAGGGGACAATGCCCCG-----Query Match

31,18; Score 1195; DB 5; Length 9266;
Best Local Similarity (81,38) Pred. No. 2.9e-294;
Matches 1568; Conservative 0; Mismatches 216; Indels 144; Gaps 2243 (2543 2183 2303 2423 2483 2603 8 g 유 8 8 ò 유 ò 셤 à 셤 ò ò 셤 ò ద ò à

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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2341 CACTACTCGAGCCACCTGAAGCGGCACATGCAGACACACAGCGGGGAGAAGCCGTTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3649 TCAGGGG-CCATATAGACCAGGGA-CTTGTCTTAGCTCACGTACCAGATGAGCTAAGT
                                       GATTAGGGCCTTGGATTCACCGCCACTCCTCCCAGAGGCTATGGATGAACTGGTTGGGAG
                                                                                                                                                                                  3767 -CIGCCCAGCCTITIAC----TGTTTTAACTTATTTCAGTGCTTTATAATAAAGGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel human secretory or membrane proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS4071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1456 BP; 287 A; 495 C; 406 G; 268 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
29.0%; Score 1115.2; DB 7; Length
Best Local Similarity 87.4%; Pred. No. 2.8e-274;
Matches 1305; Conservative 0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1126; 205pp; English.
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(REAS-) RES ASSOC BIOTECHNOLOGY
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24-JAN-2002; 2002US-0350435P.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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P-PSDB; ADA55197.
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2401 TGTGGCCGCTGCCGTACGCNTCAGCCCAGTTCGTCAACCTGACGGGACATACCCGCACC 2460	Oy 3481 TCACCTIGAACTAACTAGGT
CATACTGGCGAGAAGCCCTACCGTTGTCCCCACTGCCCCTTTGCCTGCAGCAGCCTGGGC	OY 3541 GCATTTTATACAAATGAACT
CACACTGGGGAGAAGCCCTACCGCTGTCCCCACTGCCCCCTTTGCCTGCAGCAGCCTGGGCCTGGGCCTGCAGCTGGGCCTCCCACTCCCTCC	Oy 3601 CCACACAGACTAACCTAGGC
181 AACCTGAGGGGGCATCAGCGTACCCAGGCGCGCCCCCACTCCTGCTCCTGGCGGGGGGGG	3660
	3719 GGATTCACCGCCACTGCT
CCAGGT CCAGGT	Oy 3778 TTTACTOTTTTAACTT
2761 TGTGGAACTGGATCCGAACCACTGCCAGAGCTACTGTTCCCTTGGACCTGCGGGGCTGT 2820 	ULT 15 58156 AAI58156 8t
2821 GGACAGGAACTGGAAGGAGGGAGGCAGCAGCTGGGAGCTGCCATGTGTGGGCGCTGC 2880 	AC AAIS8156; XX DT 22-OCT-2001 (first entry)
2881 ATGCGAGGAGGCTGGAGGGTTGCCACTGGGGGACCCCCAGGGCCCTGGTGACAAAGGC 2940 	
2941 TITGCCIGIAGITIAIGCCCCITIGCCACIACCCCAACCACCIGGCIGGCACAIG 3000 	Alzheimer's; amyotrophic chemokinetic
3001 AAGACTCACAGTGAGAAACCCTTCCGCTGTGCCCGCTGTCCATACGCCTCTGCTCAT 3060 	XX XX OCOURTS: SS. XX XX WOODSTEEDS.
3061 CTGGATAACCTGAAACGGCACCAGCGCGTCCACACAGAGAAAAGCCCTACAAGTGCCCC 3120 	MOZOUISSSIZ-MI. 26-JUL-2001.
3121 CTCTGTCCGTATGCCTGTGGCAACCTGGCCAACCTCAAGGGTCATGGTCGCATCCACTCT 3180	26-DEC-2000; 23-DEC-1999; 21-JAN-2000;
GGTGAC GGTGAC	PR 25-APR-2000; 2000US-0055317, 2000US-0055317, 2000US-00558042. PR 19-UTL-2000; 2000US-0053450. PR 03-AUG-2000; 2000US-0053450.
3241 AAACGTCATATGCTGCGACACGGGGGGAGAAGCCCTTCCGCTGTGCCACCTGGGCCTAT 3300 901 AAACGTCACATGCTGCGGCACACAGGGAAAGCCCTTCCGCTGTGCCACCTGCGCCTAT 960	19-001-2000; 19-001-2000; 29-NOV-2000;
3301 ACCACAGGCCACTGGGACAACTACAAGGGTCCATGGAGGTGCATGGCCATGGAGGCA 3360 	(HYSE-) H Tang YT, Wang J,
3361 GGAGGGCCTGGTCTCTGCCCCTGAGGGCTGGGCCCCACCTCATAGCCCACCCTCTGTT 3420 	WPI; 2001-442253/47. P-PSDB; AAM39000.
3421 TTGAGCACTCGGGGTCCAGCAGCCCTGGGTGCTACTGGTAGCAGGGCTCTTCATTCA	XX XX
	CIAIM I; SEG ID NO

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TAGAAACCACCTTTCCCTTTCTCCCCGCTGGTCAGGGCT 3600
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                                                                                                                                                                                                                                CCAGAGGCTATGGATGAACTGGTTGGGAG-CTGCCCAGCCT 3777
3481 TCACCTTGAACTAACTAGGTTCTTTTACCTGGGGCTCTAGGAATTAGCCCTATGCCTCT 3540
                             CACTATAAGGACCAGCCCAACCCCATGGGCGGGGGGGCCCA 1283
                                                                                                                                                                                            SCCTTGACTGAGGCACTTCATGAGCTCAGTGAGAAGGGCCCT 1343
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Zhang J, Zhao QA;
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GCCCCACCTCATAGCCCACCCTCTGTTTTGAGCTCTCGGGGCCCCACCAGCCCTGGGGACT 1203

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous not localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic coullisation of the activities such as: Immune system suppression, Activin/inhibin activity, chaemcatic/chemokinetic activity, haemostatic and thrombolytic activity, cancer disanosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form

Sequence 1558 BP; 331 A; 456 C; 494 G; 277 T; 0 U; 0 Other;

7; 45; Gaps Query Match
21.2%; Score 815.2; DB 4; Length 1558;
Best Local Similarity 85.7%; Pred. No. 1.4e-197;
Matches 1004; Conservative 0; Mismatches 123; Indels 45;

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3034 GCCCGCTGTCCATACGCCTCTGCTCATCTGGATAACCTGAAACGGCACCAGCGCGTCCAC 3093 GCCCGCTGTCCTTATGCCTCTGCTCATCTGGATAACCTGAAACGGCACCAGCGCTCCAT ACAGGAGAAAAGCCCTACAAGTGCCCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAAC 3094 785

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3393 1143

3691 1526 3751 1467 CABACCGGCTGGGGGGACTGCCAGCCTCCCACTGTTTAACTTATTCAGTGCTTT 1290 ---TITCTCCCCCGCTGGCCAGGGGTCCACACAGACTAACGTAGGCACTATAAGGACCA 3634 GCCTGAATCCCATGGTCAGGGGG-CCATATAGACCAGGGGA-CTTGTCTTAGCTCAGGTA 1347 gecenacedearegecegegegecelararegaceagedearearegecentecerreacteaged 1407 crrcacgagercagreagaaggecererarreacerecaereceeeeeeerg 3752 TGAACTGGTTGGGAG-CTGCCCAGCCTTTTAC----TGTTTTAACTTATTTCAGTGCTTT 3574 CCCTTTCTCCCCCCCCCGCTGGTCAGGGCTCCACACAGACTAACCTAGGCCACTATATGGACCA 3692 CCAGATGAGCTAAGTGATTAGGGCCTTGGATTCACCGCCACTGCTGCGAGGCTATGGA 3514 GCTCTAGGAATTAGCCCTATGCCTCCTGCATTTATACAAATGAACTAGAAACCACCTTT 1204 gérescasacessererecacacacacrearecresac---1527 ATAATAAAGGAAACACTAACAAAAAAAAAA 1558 1242 8 8 8 8 8 8 음 중 셤 ò g ò g ò

completed: May 13, 2004, 23:07:59 te : 1399 secs time

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3847 bp DNA CNRE binding factors and uses thereof. BD234712

RESULT 1 BD234712 LOCUS DEFINITION ACCESSION VERSION VERSION SOUNCE SOUNCE

BD234712.1 GI:33044482 JP 2002516664-A/6. Mus musculus (house mouse) Mus musculus

ALIGNMENTS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3847)
Chen, Y.E., Horiundi, M., Dzau, V.J. and Tamura, K.
CNRE binding factors and uses thereof
Patent: JP 2002516664-A 6 11-JUN-2002;

REFERENCE AUTHORS TITLE JOURNAL

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	34712 CNRE	1722 CNRE	1713 CNRE	18	1721 CNKE DIN	458 Sequence	933 Homo s	282 Homo s	1856 Sednen	987	0650 Homo 8	1442 Seguen	5765 Homo B	2219 Rattus	9067 Kattus	3541 Seguen	3379 Seg	383 Mus mu	39004 Mus	1541	1719 CNR	1541 Mus	2405 87 human	22083 Katt	HOMO HOMO	1714 CNRE	1715 CNRE	1720 CNR	1717 CNRE	3960 Seque	1386 Homo a	7361 Homo s	5059 Sequer	2061	0057 Homo 8	7593 Homo 8	1657 Novel	1595 Novel g	3543 Sequence	178 CNKE DI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 GGTGTGACAACATGACGTGCATCATCATTTGTTTCAAGCCCCGAAACACAGTAGAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGCAGAGAGTGGCAAGAGGAAACTGGAGGAGGCACTGTCCACGGAGGGGCTGAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGACTGTTTTCTGAGCCCTTGGACCCGAGACTGAGTTTTGTCCTTTTAGCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAGTGACTTTGATTAAAANGGNGGTTNTTTCTTCATTTCCCAGATGTAGCCTGGGCTTC
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/db_xref="taxon:10090"
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Web site: http://www-seg.wi.mit.edu
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SE (bases 1 to 19928)

BITTEN, B. Linton, L., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Brana, N., Bastien, V., Bloom, T., Boguslavkiy, L., Chang, J., Campoplano, A., Chang, J., Chago, J., Chagaraco, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farchara, S., Gardgan, G., Gardgan, G., Gardgan, G., Gardgan, S., Gardyan, S., Gardgan, W., Gage, D., Gand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Landarares, R., Landers, S., Grones, C., Kamat, A., Kartes, A., Kells, C., LaRocque, K., Lanazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., MacLean, C., Macdonald, P., Major, J., Marquis, N., MacCarthy, M., McCarthy, M., McZernan, P., MacKernan, K., Meldrim, J., Mitcol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olliver, J., Resecti, M., Ray, S., Sander, S., Schuuback, R., Schauer, S., Schuuback, R., Saman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Straus, M., Travis, M., Travis, N., Travislio, J., Travis, C., Volassiliev, H., Viel, R., Vo, A., Milson, B., Wuman, D., Ye, Wyang, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
AC114619 199296 bp DNA linear HTG 06-JUN-2002
Mus musculus clone RP24-86123, WORKING DRAFT SEQUENCE, 15 ordered
                                                                                                                                                                                                                                                                                                                                                                                              Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L (bases I to 199296)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-86123
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All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                       AC114619.2 GI:21327612
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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               LOCUS
DEFINITION
                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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* NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. Gaps between the contigs are represented as current of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* Tas contig of 1201 bp in length

* 2030 2122; gap of 100 bp

* 2030 2122; gap of 100 bp

* 3904 6031: contig of 1248 bp in length

* 6052 6181; gap of 100 bp

* 6052 contig of 2148 bp in length

* 6152 10082: contig of 2148 bp in length

* 6152 10082: contig of 3331 bp in length

* 10183 18316: contig of 8134 bp in length

* 10183 18316: contig of 8134 bp in length

* 10183 18316: contig of 8134 bp in length

* 12115 27114: contig of 8698 bp in length

* 27115 2714: gap of 100 bp

                                                           Contact: sequence_submissions@genome.wi.mit.edu
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/note="assembly_fragment"
10183. .18316
                    ------- Project Information
Center project name: L24325
Center clone name: 86_1_23
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/note="assembly_fragment"
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CNRE binding factors and uses thereof
Key Location/Qualifiers
source 1..2651
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Best Local Similarity 99.7%;
Matches 2643; Conservative
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2651)

S Chen, Y. E., Horiuchi,M., Dzau, V. J. and Tamura, K.
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THE BRIGHAM AND WOMEN'S HOSPITAL INC
OS Mus musculus (mouse)
PP D 11-JUN-2002
PP 11-JUN-2002
PP 23-APR-1999 UP 2000545541
PR 23-APR-1999 UP 2000545541
PR 24-APR-1999 UP 2000545541
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AGIP9/00,AGIP9/04,AGIP9/12,AGIP43/00,CO7K14/47,C12N1/15,C12N1/
19,C12N1/21,
C12N5/10,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,C12N15/00, PC
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JP 2002516664-A/16.
Mus musculus (house mouse)
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/organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
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Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Cardenas, V., Chavez, D., Chen, G., Chen, T., Center, A.,
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Cloveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Dermo, C., Dinh, H., Divya, K.,
Braper, H., Dugan-Rocha, S., Dunn, A., Dinh, H., Divya, K.,
Fernandez, S., Fihley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garrer, T., Garza, M.,
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Gunaratne, P., Haaland, W., Handel, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
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Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J.,
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                                                CATCTGGATAACCTGAAACGGCACCAGCGCGTCCACAGGAGAAAAGCCCTACAAGTGC
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Direct Submission

All Submitted (16-SEP-2001) Human Genome Sequencing Center, Department Submitted (16-SEP-2001) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Skat Genome Sequencing Consortium.

Direct Submission

AL Submitted (13-NOV-2002) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:22856068.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fature table balow represents a scaffold, in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filed with Ns to the serimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
               * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a "working draft" sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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54.48; Score 2092; DB 2; Length 2
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----CITAACTCCTGAGTAAGCAGCCCGCTGGAGGCCATCCT-GCGCTGTTCGCCTTCAG
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                                                                                                                                                                                     AGGACATTCTTTTTTTTGGGGGCTCTGTGACCCCTAGCCGCTTGCACCCGCTCTGTTT
                                                                                                                                                                                                                         AGGACATTCTTTTTATTATTGGCGGCTCTGTGACCCCTAGCCGCTTGCACCCGCTTGTTTTT
                                                                                                                                                                                                                                                                                             GTACACTITICAAGCAACACTITITICAGACTAAAGGCCAAACAAAAGGCTAATCGTGCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                 AGTGTCATGCTTTACTCTCCTACCCTGGCCCCATATGTGGTGGGCGGCTGTTGCTGCATG
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OY 2217 AGCTGTCAGCTGTGGGGGGCCGACAC Db 262333 AGCCTGTCAGCTGTGGGGGGCCGACAC Qy 2277 GGGTGGGGGGCCCCGCTGC Db 262273 GGGTGGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Db . 262213	2449	2509	Db 262033 AGCAGCCTGGGCAACCTGAGGCGGCTC	DD 261973 TGCCAACCTGTGGTTTCCGATGCTGTG OY 2629 GAGCAGGAGGGAACAATGCCCCGACGAT	Db 261913 GAGCAGGAAGGACAATGCCCCGGCGAT	261853	261793	Db 261733 CCAGATTGTGGGCAGCTGCGGGGTGAAG	Oy 2782 CTGCCAGAGCTACTGTTCCCTTGGACCT	Oy 2842 GAGGGAGCAGGCTGGGAGCTGCCATGT			Db 261493 TTTGCTACTCACTACCCCAACCACCTGG Qy 3022 CCCTTCCGCTGTGCCGCTGTCCATACG	261433	261373	Db 261313 AACCTGGCCAACCTCAAGCGTCACGGTC
GTGCAGTTCACAACAGCTGGCTCCCTGGTTCGAATTATGGGAACGGCTTGTGAGGGAGAT TCCACAAGCACCCTCCCTTTAGTGGATACTCAAGATTCCTTCGACGAAGGTCCTGGG	2014 GAAGAGGATGAAGGCGCCACAACCAGCTCATGAGAGAGACTTTGAGAGAGA	263233 GGTGTGTTAAAGGGTCGTGGTTAAGGATAAGAGCCTTTTGGTAACTCAAGCCCTTTAGAA 263174 2073 2072	263173 GGCGGTGTTAGCGACCAAAACACCACTTCTTTTACAACCTAGCAGCAGTTTTGGTGA 263114	GITGAAGITCTGGGTCCGGGCTAAAGGTGGTGTGAATACAAGGGTGGGT	TTATGTACCCCTCAAGAGGTTCATGGAAGGGAATTATGTAAATAAGCTACTCTTAAAACT	2073	262933 CTCCTCGTTTATTTCTTGGGTATTTTTTAAAGTCAGAGAAACCATATAAAAGAATCTGC 262874	2073 2072 262873 CCTTTCTGTGTAATTTGCACTACATTGCTCCCACTTTCTCCCAAATTGTGCCTACTTGAGA 262814	SV SIDILIVITY OF STATE S	262813 TGGCTTTCATTACATATCAGCCTTATATAAAAGGGCCCTTACTACTACTAAACCAGGGTTTACA 20273*	262753 AAAAAGATCTTGGGGGTCTTTATATTTTTACTTATCTCATATTGTTGCTTCACATCAGCCT 262694 2073 2072	262693 GTACTCCACTTCAAGCCTGTGATATTTTCCATTTGTTGGAAATGATAAGTCACCCTAGT 262634	262633 GTTAGTAATTAGGCTCAAATAGAATGAAATCAAAGGTGAGGCAGAATAAGTGGGGGCTTTT 262574	TGTGAGAAATGAGAATTTGGAACTCAGTCTTGAGCCATGTTGATTGGTTTCTTTTTT	2073	2097 TGGACTTCCCTATGGGCTGAGTGACGAGTCTGGGGGCGGCGCGCGC	2157 GAGTGAAGTTGAGGAACCAGCCAGGGGTCCAGGGAGGGGGGGG
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	2217	AGCCTGTCAGCTGTGTGGGGGCCGACAGGTGAGGGCCGTGTTGTGGGGCAGGAGGCG 2276 	4
	2277	GGGTGGGGGGCCCCGCTGCCCCCACGTTACTGTACTCTATGCCGGCTGTGC 2328 GGGTGGGNNNNNNNNNNNNNNNNNNNNNN	ঝ
	2329	GCTTTCGTGTCCCACTACTCGAGCCACCTGAAGCGGCACATGCAACACACAC	4,
	2389	AAGCGTICCGCIGIGGCCGCIGCCCAIACGCNTCAGCCCAGITCGICAACCIGACGCGA 2448 	4
	2449	2508	4
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	2629	GAGCAGGAGGACAATGCCCCGACGATCAGA	4.
	2661	¥	
	261853	actggtaggtaggagagagatacttggattaatggcccatatctcattgttcccaca 261	4
	2662	ATGCGCTGATCCTGCCGGACTTGAGTCTTCATGTGCCGCCGGTGGTGCCGGTTCCTG 272	4.
	2722	CTGTGGGCAGCTGCGGGGTGAAGGGGGAGCTTGTGTGGAACTGGAACCA 2781 	74
	2782	TGTTCCCTTGGACCTGCCGGGCTGTGGACAGGAACTGGAGGGT 2	14
	2842	ascagcagcagcagcasccargragagcgcracaracaagagagaggaggaggaggaggaggaggaggaggagga	
	290	GGGGGACCCCAGGGCCCTGGTGACAAAGGCTTTGCCTGTAGTTTATGCCCC 296	
	296	SCCACTCACTACCCCAACCACCTGGCACATGAAGACTCACAGTGGTGAGAAA 3021 	
	302	TCCGCTGTGCCCGGCTGTGCGCCTCTGCTCTGGATAACCTGAAACGGCAC 3081	
_	261433	cerrececrerecececrerearacecercrecearascaraacereaaaceceae 2613	74
	3082	CAGCGCGTCCACAGGAGAAAAGCCCTACAAGTGCCCCTCTGTCCGTATGCCTGTGGC 3141	14
	314	AACCTGGCCAACCTCAAGGCGTCATGGTCGCATCCACTCTGGTGACAAACCTTTCGGTGT 3201	24
^	261313	AACCTGGCCAACCTCAAGCGTCACGGTCGTATCCACTCTGGTGACAAACCTTTTTCGGTGT 2812	

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/organism='Mus musculus (mouse)'.
AGIK37/48,C12N5/00
CNRE binding factors and uses thereof
Key Location/Qualifiers
1. 2336
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260896 GAAAACCATTTCCCTTTCTCCCCGGTGGTCAGGGGCTCCACAGAGAGTAACCTAGGC 260837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260778 TTGGCTCATGTACCTGATGAGCTAAGTGATTAGGACCTTGGATTCACGCCACTGCTCCC 260719
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                                                                                           261253 AGCCTTTGCAACTACAGCTGCAACCAGAGCATGAACCTCAAACGTCATATGCTGCGGCACAC 261194
                                                                                                                                                                                                 261133 TACAAGCGTCATCAGAAGGTGCATGGCCATGGTGGAGGAGGAGGCCTGGTCTCTCTGCC 261074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261073 CCTGAGGGTFGGGCCCCACCTCATAGCCCACCCTCTGTGAGCACTCGGGGGTTCAGCC 261014
                                                                                                                                                                                                                                                                                         TACAAGCGTCATCAGAAAGGTGCATGGCCATGGTGGAGCAGGAGGGCCTGGTCTCTCTGTGCC 3381
                                                                                                                                                                                                                                                                                                                                                                                                            CCTGAGGGCTGGGCCCCACCTCATAGCCCACCCTCTGTTTTGAGCACTCGGGGTCCAGCA 3441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3621 ACTATATGGACCAGCCTGAATCCCATGGTCAGGGGCCCATATAGACCA-GGGGACTTGTC 3679
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PN 19-202516664-A/15
PN 11-0022516664-A/15
PP 21-APR-1999 UP 2000545541
PR 24-APR-1999 US 60/082997
PY 19-202516054541
PR 24-APR-1999 US 60/082997
PC CIZNIS/09, A6IR31/711, A6IR38/00, A6IR48/00, A6IR48/00, PC A6IR48/00, A6IP9/04, A6IP9/12, A6IP43/00, CO7K14/47, CIZNI/15, CIZNI/PC CIZNI/21, PC                                  3202 AGCCTTTGCAACTACAGCTGCAACCAGAGTATGAACCTCAAACGTCATATGCTGCGACAC 3261
                                                                                                                                                           3262 ACGGCCAGAAAGCCCTTCCGCTGTGCCACCTGCGCCTATACCACAGGCCACTGGGACAAC 3321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3502 CTTTTACCTGGGGCTCTAGGAATTAGCCCTATGCCTCCTGCATTTTATACAAATGAACTA 3561
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Chen, Y.E., Horiuchi, M., Dzau, V.J. and Tamura, K.
KNEE binding factors and uses thereof
Patent: JP 2002516664A 15 11-JUN-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL INC
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Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1378 ACGGAGGTACCAGCTGGTCTTCGGAGGGGGGTAGGGGGCTCCATGAATGGAAGCGGCGGC 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1917 AGTGGATACTGAAGATTCCTTCGACGAAGGTCCTGGGGCCCTGGTGTTGGAGAGCGATTT 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1977 GCTACTAGGCCAAGATCTGGAGTTTGAAGAGAAGAAGAAGAAGAGATGAAGGTGACGGCCA 2036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2037 CAACGACCAGCTCATGGGCTTTGAGAGACTCTGAAGGAGACTCTCAGGGGGCCAGACC 2096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1318 TGTACAGCCCATGAACTACGCATCCCGTGTTGCTCTGCGGTGGCGGAAGCGGAAGCGGGT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1617 TGCCCCGAAGGAAGCAAAGCCATCCACAGCCCGTGAAATGCGAGGGGGTCAAAGGTCAGG 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ACGGAGGTACCAGCTGGTCTTCGGAGGGGGGTAGGGGGCTCCATGAATGGAAGCGGCGGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 GCTACTAGGCCAAGATCTGGAGTTTGAAGAGGAAGAAGAGGAAGAGGATGAAGGCCA 840
                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATTGGTTGGCTAGCAGCGCATCACAATCACTTCCTGGTCATGCTGCTACTGCGCTCCGGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TGTACAGCCCATGAACTACGCATCCCGTGTTGCTCTGCGGTGGCGGAAGCGGAAGCGGGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 GGTGGAGGGGACTCCTGAGGGTTAGGGGCGGATGATCTGGGATCTTCGCTCCTTACCAG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 CTTGGTTCGGATTATGGGTACTGCTTGGGAGGGAGTTCCACAAGCACCCTCCCCTCTTT 720
                                                                                                                                                                                                                              1 AIGGAGGGGGGGACCACCTTCCTGGTTGGCTTGGGTTACGCTCCAGCTTCTG
                                                                                                                                                                                                                                                                                                                                         1258 ATTGGTTGGCTAGCAGCGCATCACAATCACTTCCTGGTCATGCTGCGACTGCGCTCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1438 GGCGGCGGGAGCGACCTGAGCTGGATTCCGGGGCCGGGGG-CAGGGGCTGCCCAGGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 CACCGGGTATATGGGGGGGGGGTTCGTGGATCCTAAGAGCAAGGACCGACGGAGGGCCGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1557 GGGAGGGGCGGGGCGGAGGCCTCGGGCCGGAAGCGCGTCGGGCTGGAGCCGGTCACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     721 AGTGGATACTGAAGATTCCTTCGACGACGACCTGGGGGCCCTGGTGTTGGAGAGGTTT
                                                                                        7; Indels 316; Gaps
Query Match 51.7%; Score 1988.4; DB 6; Length 2336; Best Local Similarity 87.8%; Pred. No. 0; Matches 2328; Conservative 0; Mismatches 7; Indels 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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1496

1666 1666 1666 1667	RESULT 7 BCO58976 BCO58976 BCO58976 BCO58976 MUS musculus RIKEN cDNA D430028M17 gene, mRNA (cDNA clone MGC:67303 INAGES:5685033), complete cds. BCC58976.1 GI:37589246 WGC58976.1 GI:37589246 WGCS810N WGC BCO58976.1 GI:37589246 WGANISM WGC BCO58976.1 GI:37589246 WGANISM WGC BCO58976.1 GI:37589246 WGANISM WGC BCO58976.1 GI:37589246 WGANISM WGARACOA, Chordata, Craniata, Vertebrata; Euteleostomi; Musculus Euteryota; Rodentia; Sciuncognathi; Muridae; Murinae; Musculus Euteryota; Rodentia; Sciuncognathi; Muridae; Murinae; Musculus Straubberg, E.J. Feingold, E.A., Grouse, L.H., Derge, J.G., Rausner, R.D., Collins, F.S., Wagner, L., Schemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schemen, C.F., Brant, N.K., Hoppin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Gravant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Gravant, T.L., Stapleton, W., Scares, M.B., Bonaldo, M.F., Gravant, T.L., Scherk, J.C., Scherk, S.C., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bogaak, S.A., McEwan, P.J.,
10	2817 CTGTGGACAGGAACTGGAGGGGGGCAGCTGGGGCTGGCCATGTGGGGC 2876 1485

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2817 CTGTGGACAGGAACTGGAGGAGGAGGTGAGGGCAGCAGGCTGGGAGCTGCCATGTGTGGGGCG 2876
   jsmilkrhmlrhtgekpfrcatcayttghwdnykrhûkvhghggaggpglsapegwap
                                                                                                   COG5048, FOG: Zn-finger [General
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1026 GCCACCAGGTGCCAGTTTCCTGCCAGACTGTGGGCAGCTGCGGGGTGAAGGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2217 AGCCTGTCAGCTGTGTGGGGGGCCGACAGGTGAGGGGCCGTGTTGTGGGGCAGGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   906 CTGIGGCTITCGATGCTGTGCTCCCACGACCAACCCGGCCTCCCAGTCCCACAGAGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                966 GGGGACAATGCCCCGACGATCAGAAGATGCGCTGATCTTGCTGCCAGACTTGAGTCTTCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1086 cridrendaacresarccearccacreccasacracrerrecriresaccresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                726 cederieredecederadecerradecercaderederedaderadecedadaradece
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGTGGCTTTCGATGCTGTGCTCCACGACCAACCCGGCCTCCCAGTCCCACAGAGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2277 GOGTGGGGGCCCCCGCGCCCCCACGGTTACTGTACTCATGCCGGCTGTGCGCTTTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACGACCAGCTCATGGGCTTTGAGAGGACTCTGAAGGAGACTCTCAGGGGCCCAGACC
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                DB 10; Length 2220;
                                                                                                                                                                                                                                                                                                                                 8; Indels
                                     PHSPPSVLSTRGPAALGATGSRALHSDSP"
1432. .1653
/note="COG5048; Region: COG504
Eunction prediction only]"
/db_xref="CDD:COG5048"
                                                                                                                                                                                                                                                                Score 1918.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.6%;
Matches 1923; Conservative (
                                                                              misc_feature
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.

Location/Qualifiers

1. .220
/organism="Mus musculus"
/pre="mRNA"
/pre="mRN
MCKernan, K.J., Malek, J.B., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Halton, E., Keteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevohenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Sutterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, J.B., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences

B. 22388257

B. 22388257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-0CT-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Email: agapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
PC Cancer Agency, Vancouver, BC, Canada
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AX834458 LOCUS DEFINITION Sequence 1582 from Pat ACCESION AX834458 VERSION AX834458 AX84458 AX84458 AX84458 AX84458 AX84468 AX	TITLE Full-length cDNA seque JOURNAL Patent: EP 1347046-A Research Association for source Source 1 . 2013 Mol Lype="unity for style="unity for style" Mol Lype="unity for style="unity for style" Mol Lype="unity for style="unity for style="unity for style="unity for style="unity for style="unity for style" Mol Lype="unity for style="unity for style="unity for style" Mol Lype="unity for style="unity for style-"unity for style="unity for style-"unity for style-"unity for style="unity for style-"unity for style	ORIGIN Query Match Best Local Similarity 88.6%; Matches 1727; Conservative Qy 1885 GAGGGAGATTCCACAAGCA	102 GAGGAGAATCCAC 1945 GGTCCTGGGCCT 162 GGACCGGGGCCT 162 GGACCGGGGGCCT	2005	Qy 2125 GAGTCTGGGGGCGGCGCGCG Db 342 GAGTCTGGGGGCGGCGGGC Qy 2185 CCAGGGAGGCCAGGGGTG Db 402 CCAGGGAGGCCAGGGGTG	Oy 2245 GGTGAGGGCCGTGTTGTG	Oy 2365 CACATGCAGACACAGGG Db 582 CACATGCAGACACAGGG Oy 2425 GCCCAGTTCGTCAACCTGA Db 642 GCCCAGTTCGTCAACCTGA	2485 TGTCCCCACTGCCCTTTG
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oligo capping, fis (full insert sequence).
Homo sapiens (human)
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Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujil,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
NEDO human cDNa sequencing project
Unpublished
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CTACTGTACTCATGCCGCCTCTGCACCTTCGTGTCCCACTACTCGAGCCACCTGAAGCGG CACATGCAGACACACAGCGGGGAGAAGCCGTTCCGCTGTGGCCCGCTGCCCATACGCNTCA CACATGCAGACACACAGGGGAGAGAGCGGTTCCGCTGTGGCGGCTGTGCCCCTAGGCCTCA <u> Gereaadecerarieradodecadadadeceadareadeceeeceeraceadeceeades</u> Tracteracteraceceecretececriticereceaciteaeceaccidaaecee 2425 642 2485 2 ñ Ŋ 55 582 \$ 8 \$ 8 8 8

GCCCAGITCGICAACCTGACGCGACAIACCCGCACCCAIACTGGCGAGAAGCCCIACCGI TGTCCCCACTGCCCTTTGCCTGCAGCCTGGGCAACCTGAGGGGGGCATCAGCGCACC

CACACAGGGCCTCCCACCTCCTCCTGCCCAACCTGTGGCTTTCGATGCTGTGCTCCACGA TGTCCCCACTGCCCTTTGCCTGCAGCCTGGGCAACCTGAGGCGGCATCAGCGTACC 2545 762 702

GCGCTGATCCTGCCAGACTTGAGTCTTCATGTGCCACCAGGTGGTGCCAGTTTCCTGCCA CCAACCCGGCCTCCCAGTCCCACAGAGCAGGGGGACAATGCCCCGGACGATCAGAAAAT 2665 2605 822

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CCAGAGCTGCTATTCCCTTGGACCTGCCGGGCTGTGGACAAGAGGTGGAGGAGGTGAG

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CCAGAGCTACTGTTCCCTTGGACCTGCGGGGCTGTGGACAGGAACTGGAGGAGGGTGAG

GGCAGCAGGCTGGCATGTGTGTGGGCTGCATGCGAGGAGGAGGCTGGAGGGCTTT

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GCCACTCACTACCCCAACCACCTGGCTCGGCACATGAAGACTCACAGTGGTGAGAAACCC

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Score 1518; DB 9; Pred. No. 0; 0; Mismatches 178;

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CTGGCCAACCTCAAGCGTCATGGTCGCATCCACTCTGGTGACAAACCTTTTCGGTGAAG CTTTGCAACTACAGCTGCAACCAGAGTATGAACCTCAAAACGTCATATGCTGCGACACACG CTTTGCAACTACAGCTGCAACCAGAGCATGAACCTCAAACGTCACATGCTGCGGCACACA GOCGAGAAGCCCTTCCGCTGTGCCACCTGCGCCTATACCACAGGCCACTGGGGACAACTAC 1422 1362 3205 3265 1482

CTGGCCAACCTCAAGCGTCATGGTCGCATCCACTCTGGTGACAAACCTTTTCGGTGTAGC

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<u> Aagceccaccadaaadererareeccaceereegecaagaageccreercrectecrer</u> AAGOGTCATCAGAAGGTGCATGGCCATGGTGGAGCAGGAGGGCCTGGTCTCTCTGCCCCT 3325 1542

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1602 GAGGGCTGGGCCCCACCTCATAGCCCACCTCTGTTTTTGAGCTCTCGGGGCCCACCACCAGC GAGGGCTGCGCCCTCATAGCCCACCCTCTGTTTTGAGCACTCGGGGGTCCAGCCC cressaacrescrescesecrerecacacacacacacrearcersaac----3385 3445 1662

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TATGGACCAGCCTGAATCCCATGGTCAGGGG-CCATATAGACCAGGGGA-CTTGTCTTA 3682 TAAGGACCAAGCCCATGGGGGGGGCCCATATGGACCAGGGGACCTTG 1749 gccacchi----rinchcccccccacacaccacaccacacacacacacacacaa 1805 3625

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CAGIGCITIAIAAIAAAGGAAACACIAAC

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CAGTGCTTTATAAAAGGAAACACTAAC 3826

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linear mRNA ď 2159

PRI 08-0CT-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               734 coecretedecectedecectracecercaececececececercaecereaececeaeaearaece
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/note="COSS048; Region: COGS048, FOG: Zn-finger [General function prediction only]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 GCTACTAGGCCAGGATCTGGAGTTTGAGGAGGAAGAGGAAGAGGAGGAAGGCGACGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 GGGTGGGGGGCCCCTGCTGCCCCCACGGCTACTGTACTCATGCCGCCCTCTGCACCTTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1917 AGTGGATACTGAAGATTCCTTCGACGAAGGTCCTGGGGCCCTGGTGTTGGAAGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1977 GCTACTAGGCCAAGATCTGGAGTTTGAAGAGGAAGAGGAAGAGATGAAGGTGACGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.1%; Score 1505.8; DB 9; Length Best Local Similarity 88.5%; Pred. No. 0; Matches 1716; Conservative 0; Mismatches 178; Indels
                                                                                                                                   db_xref="LocusID:130557"
                                      'note="Vector: pOTB7"
'lab host="DH10B-R"
                                                                                                gene="FLJ32203"
                                                                                                                                                                                                                     codon_start=1
                                                                     .2159
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Contact: MGC help desk
Contact: MGC help desk
Email: cgapba-ramail.nlh.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Conscrtium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing py: National Institutes of Health Intramural
Sequencing Maryland;
Web site: http://www.nisc.nih.gov/
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., (Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 2159)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleron, M., Soares, M.M., B., Bonaldo, M.F., Casarant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abrameson, R.D., Mullahy, S.J., Boask, S.A., McZwan, P.J.,
McKernan, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wanzny, D.M., Sodersyen, E.D.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse order Sci. U.S.A. 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linia at: http://image.llnl.gov Series: IRAL Plate: 47 Row: d Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24432061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (02-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Homo sapiens hypothetical protein FLJ32203, mRNA (cDNA clone MGC:59968 IMAGE:5467936), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="WGC:59968 INAGE:5467936"
/tissue_type="Skin, melanoma, amelanotic"
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/db_xref="taxon:9606"
                                                                                 BC052282
BC052282.1 GI:30354479
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                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
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           DEFINITION
                                                                             ACCESSION
VERSION
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SOURCE
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MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
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COMMENT
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Azimzai, Y., Bandman, O., Tang, Y.T., Mathur, P., Shah, P., Au-Young, J.
and Reddy, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 88.6%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 176; Indels
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| Organism="Homo sapiens"

| Mol_type="unassigned DNA"

| Ab xref="caxon:9606"

| Note="incyte ID No: 870100CB1"
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Incyte Genomics, Inc. (US)
Location/Qualifiers
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Sequence 121 from Patent WO0172777.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                       Query Match
Best Local Simi
Matches 1598;
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3680

1721

1781

1841

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505] .2520
note="similar to Homo sapiens BST AW327943 (NID:g6798438)
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hote="similar to Homo sapiens EST AW327944 (NID:g6798439)
                                                                                                                                              A transpaon exists in the growth of this clone which has been deleted from the finished sequence. This transposon would insert after base 78210. Unsure bases exists between bases 165498 to 165505. Un unresolved trandem repeate exists between bases 4700 to 6435. Polymorphisms have been identified between AC009427 and AC074117. Data from AC009427 was used to finish this clone,
                                                             NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RPI1-413M20;
actual end is at base position 195880 of RPI1-413M20.
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/note="CpG island (%GC=74.2, o/e=0.70, #CpGs=131)"
5543. .5910
/rpt_family="SVA"
5926. .5950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11537. .3202
note="similar to Homo sapiens EST AU130518
and coworkers at http://www.chori.org
VECTOR: pBACe3.6
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/rpt_family="(TTTTA)n"
3953. .3995
/rpt_family="MER1_type"
3962. .3990

    .195880
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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4285. .4331
/rpt_family="MER1_type"
4515. .4593
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4780. .6423
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rpt_family="MER1_type"
646. .3952
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/rpt_family="AT_rich"
2959. .3251
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="AT_rich" 996. .4284
                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="RP11-413M20"
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1. .207
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/rpt_family="Alu"
1518. .1538
/rpt_family="(A)n"
1546. .1866
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/rpt_family="Alu"
501. .647
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221
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1558. .3645
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map="2"
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Mapping information for this clone was provided by Dr. John D.
Mapping information of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (08-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (Dases 1 to 195880)
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Submitted (01-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (05-FEB-2002) Genome Sequencing Center, Washington
Submitted (05-FEB-2002) Genome Sequencing Center, Washington
Modification of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63109, USA
6 (bases 1 to 195880)
                                                                                                                                                                                                                                                              Submitted (14-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this close. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 195880)
Sun, H., Kozlowicz, A. and Dignan, G.
The sequence of Homo sapiens BAC clone RP11-413M20
Upublished (2001)
3 (bases 1 to 195880)
Haterston, R.H.
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                           Ioward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
         Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                        MO 63108, USA
5 (bases 1 to 195880)
Waterston, R.H.
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Waterston, R.H.
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                                                                                                                                                                                                                                                Direct Submission
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/rpt_family="GC_rich" repeat_region 5968 6960 /rpt_family="gVA"	, da	2363 GGCACATGCAGACACACAGGGGGAGAAGCCGTTCCGCTGTGGCCGCTGCCCATACGCNT 2422
<pre>repeat_region 62936345 /rpt_family="GC_rich" repeat_region 69426971 /rpt_family="(A)n"</pre>	g g	2423 CAGCCCAGTTCGTCAACCTGACGCACATACCCGCACCCATACTGGCGAGAAGCCCTACC 2482
repeat_region 70857209 / Trpt_family="L2" repeat_region 72107518 /rpt_family="Alu"	Q da	2483 GTTGTCCCACTGCCCCTTTGCCTGCAGCAGCCTGGGCAACCTGAGGCGGCATCAGGGC 2542
<pre>repeat_region 76667800 /rpt_family="MER1_type" repeat_region 90579346 /rpt_family="Alu"</pre>	g ç	2543 CCCACACAGGGCCTCCCACTCCTGCCCAACCTGTGGGTTTTCGATGCTGTGCTCCAC 2602
<pre>repeat_region 989910049 /rpt family="L2" repeat_region 100291071 /rpt family="(TA)n"</pre>	à 8	2603 GACCAACCGGGCTCCCACACAGAGCAGGAGGGGACAATGCCCCGACGATCAGA 2660
repeat_region 1010710354 /rpt_family="il" repeat_region 1035510533 /rpt_family="WRRT type"	\dot \dot \dot \dot \dot \dot \dot \dot	2661 2660 167602 GTAAGACACACGAGGACCAAAGATCTTGGGACATGGGTGGCTGACCCTAGGAATGCTTG 167661
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<pre>repeat_region 11179 .11483</pre>	ර යි	2688 TCITCAIGIGCCACCAGGIGGIGCCAGITICCIGCCAGACIGIGGGCAGCIGCGGGGIGA 2747
<pre>repeat_region 11484. 11602 / rpt_family="Alu" repeat_region 11633. 12618" /rpt_family="L1"</pre>	\$ Q	2748 AGGGAGAGCTIGTGGAACTGGATCCGAACCACTGCCAGAGCTACTGTTCCCTTGGAC 2807
_region 12619. /rpt_f_ _region 12673. /rpt_f	\$ a	2808 CTGCCGGGGCTGTGGAACAGGAACTGAGGGGGGCAGCAGGCTGGGAGCTGCCAT 2867
., .,, .	& A	2868 GTGTGGGCGCTGCATGCGAGGAGAGGGTTGCCACTGGGGGACCCCAGGGCCC 2927
13408 6%; Score 1255.2; DB 9; Length 195880; 2%; Pred, No. 3.7e-291;	<i>ò</i> 8	2928 IGGIGACAAAGGCIIIGCCIGIAGIITAIGCCCCIIIGCCACTCACIACCCCAACCCT 2987
Conservative 0; Mismatchee GAGGAAGAAGAAGAAGATGAAGGTGAAGGCC	\$ B	2988 GGCTCGGCACATGAAGACTCACAGTGGTGAAAACCCTTCCGCTGTGCCGCTGTCCATA 3047
2063 GAGATCTGAGAGAGACTCTCAGGGGCCAGACTTCCCTATGGCTGACTGA	λ d d	
Qy 2123 ACGAGTCTGGGGGCGCCGCACTAAGTGCGGAGAGTGAAGTTGAGGAACCAGCCAG	중 음 중	CTACAAGIGCCCCCTCTGTCCTTATGCCTGTGGCAATCTGGCCAACCTCAAGGCGTCATGG
Qy 2183 GTCCAGGGGAGGCCAGGGCTGAGGCCAGGCCCAGCCTGTCAGCTGTGGGGGGCCGA 2242 Db 167122 GTCCAGGGGAGGCCAGGGCTGAGAGCCAGGCCCAGCTGCCAGCTGTGTGGGGGGGG	da da	TOGGATCCACTCTGGTGATGATCCTTTTCGGTGTGAGCCTTTGCAACTACAGCTGCAACCA
Qy 2243 CAGGTGAGGGCCGTGTTGTGGGGGGGCGGGGGGGGGCCCCCGCTGCCCCAC 2302 Db 167182 CAGGTGAGGGCGTGTTGTGGGGGGGCGGGGGGGCCCCCCCC	δλ -	GAGTATGAACCTCAAACGTCATATGCTGCGACACGGGCGGAAAGCCCTTCCGCTGTGC
	<u> </u>	3288 CACCTGGGGCTAIACCACAGGGCCCACTGGGAACTACAGGGGTCCATCAGAGGGTCCATGG 3347

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 70 Row: d Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Excellent library of
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                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                      origin.
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Homo sapiens, Similar to hypothetical protein FLJ32203, clone
IMAGE:4795511, mRNA.
                                                                                                                     CCCACCCTCTGTTTTGAGCACTCGGGGTCCAGCAGCCCTGGTGCTACTGGTAGCAGGGC 3467
                                                                                                                                                                                                                                                                          TCTTCATTCAGACTCACCTTGAACTAAGTTCTTTTTACCTGGGGCTCTAGGAATTAG 3527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CONA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1461)

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Submitted (19-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
3528 CCCTATGCCTCCTGCATTTTATACAAATGAAACTAGAAACCACCTTTCCCTTTCTCCCCCG
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AUTHORS
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                                                                                                                                              Length 1456;
                                                                                                                                           Query Match
29.0%; Score 1115.2; DB 6; Length
Best Local Similarity 87.4%; Pred. No. 1.3e-257;
Matches 1305; Conservative 0; Mismatches 144; Indels
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Yamamoto,V.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masulto,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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         GAAACGGCACCAGCGCGTCCATACAGGAGAGAAGCCCTACAAGTGCCCCCTCTGCCCTTA
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Helix Research Institute (JP); Research Association
Biotechnology (JP)
1.0cation/Qualifiers
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Search completed: May 14, 2004, 03:12:30 Job time : 14677 secs

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OM nucleic - nucleic search, using sw model Run on:

May 13, 2004, 15:37:55 ; Search time 251 Seconds (without alignments) 8505.562 Million cell updates/sec

Title: Perfect score: Sequence:

Scoring table:

682709 seqs, 277475446 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: 1365418 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ULT 1 09-620-312D-32 atent No. 658962 REMERAL INFORMATION: APPLICANT: Tang, Y: Tom APPLICANT: Tang, Y: Tom APPLICANT: Tang, Y: Tom APPLICANT: Tang, Vined APPLICANT: Tang, Vined APPLICANT: Tang, Vined APPLICANT: Chen, Rui-hong APPLICANT: Chen, Rui-hong APPLICANT: Chen, Rui-hong APPLICANT: Chen, Rui-hong APPLICANT: Chen, Rui-hong APPLICANT: Chen, Rui-hong APPLICANT: Xue, Aidong J. APPLICANT: Xue, Aidong J. APPLICANT: Xue, Aidong J. APPLICANT: Wang, Yonghong APPLICANT: Wang, Yonghong APPLICANT: Wang, Yonghong APPLICANT: Wang, Yonghong APPLICANT: Wang, Duruni APPLICANT: Wang, Linn Rui APPLICANT: PAPLICATION NUMBER: 09/488 PRIOR FILING DATE: 2000-01-21 CURRENT FILING DATE: 2000-01-21 AUWHBER OF SEQ ID NOS: 1105 APPLICATION: COS LOCATION: (50)(1174) 09-620-312D-32	21 similarity 85.	CTGCCAGACTI
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; MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO; ANTI-SENSE: NO
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CAGCTGCGGGGTGAAGGGAGGGTTGTGTGGAACTGGATCCGAACCACTGCCAGAGCTA 2793
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                                                                                                              Sequence 1, Application US/08822701
| Patent No. 5976853
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Basilico, Claudio
| TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
| NUMBER OF SEQUENCES:
| ADDRESSE: David A. Jackson, Esq.
| STREET: 401 Hackensack Ave, Continental Plaza, 4th
| STREET: Floor:
| STREET: New Jersey
| COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
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1527 ATAATAAAGGAAACACTAACAAAAAAAAAAAA 1558
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Beg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
FILEPAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1824 base pairs

"WOR: nucleic acid
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Sequence 21, Application US/08935855
Sequence 21, Application US/08935855
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: Ploor
STREET: Ploor
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APPLICATION NUMBER: US/08/935,855 FILING DATE:
CLASSIFICATION: 435
                   373 AGCIGCIGGAICAGIGCCIGGCGCCAGACACI
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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMDALIble
COMPUTER: IBM PC COMDALIble
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APPLICANT: Guthridge, Mark
APPLICANT: Guthridge, Mark
APPLICANT: Guthridge, Mark
APPLICANT: Guthridge, Mark
APPLICANT: Guthridge, Mark
APPLICANT: Guthridge
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FINI3
MUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.
ADDRESSER: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STREET: New Jersey
COUNTRY: USA
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COMPOURE: Floppy disk
COMPOURE: FROM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 8.8e-150;
0; Mismatches 2;
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APPLICATION NUMBER: US/08/935,855
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE, POCKET NUMBER: 1049-:
TELEPANTUNICATION INFORMATION:
TELEPANTUNICATION INFORMATION:
TELEPANTUN FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Patent No. 6066485
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 99.7%;
Matches 617; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: double
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US-08-935-855-1
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US-08-935-855-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGIGIGCAGGGGCTGGGCTTTCCTCAGCCCATTACAAAGAGGGCCCCCCCACCCC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACGTGCATCATCATTTGTTTCAAGCCCCGAAACACAGTAGAGCTTCAGGCAGAGAGTG 492
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                                                                                                                                                                                                                                                                                                      Query Match 16.0%; Score 615.8; DB 3; Length 2081; Best Local Similarity 99.7%; Pred. No. 9.4e-150; Matches 617; Conservative 0; Mismatches 2; Indels 0;
            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAK: 201-343-1684
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 2081 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TYPE: nucleic acid
STRANDEDNES: double
TYPE: Innear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2044 AAGGCCAAACAAAGCTAA 2062
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                            HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                            US-08-935-855-21
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RESULT 5
US-08-935-855-19
; Sequence 19, Application US/08935855
; Patent No. 6066485
; CENERAL INFORMATION:

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1552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1733 GGTATGAGGGGGAGGGGGGGGGGGGGTTCACTCCGCCCATTCCAAAGAGGGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1493 reaccrecarcarcarracarcas de constantes 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 AC---AAAAAGAAGGCCAAGAGGATTAGTGGTCAACCGGA-CCCTGCCCATGTGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 AGCTGCTGGATCAGTGCCTGGCGCCAGACACTTCTGGGGATGGTACAGGGTGTGACAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 TGACGTGCATCATCATTGTTTCAAGCCCCGAAACACAGTAGAGCTTCAGGCAGAGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
APPLICANT: Guthridge, Mark
APPLICANT: Basilico, Claudio
TILLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Rloa.
CITY: Lackensack
STATE: New Jersey
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.0%; Score 270.2; DB 3; Best Local Similarity 83.8%; Pred. No. 4.5e-60; Matches 393; Conservative 0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEPAK: 201-343-1684
INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
LENGTH: 1890 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-935-855-19
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CLONE: GENBANK
CLONE: 9189043
US-09-016-434-1229
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2405 GCCGCTGCCCATACGCNTCAGCCCAGTTCGTCAACCTGACGCGACATACCCGCACCCATA 2464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2465 CTGGCGAGAAGCCCTACCGTTGTCCCCACTGCCCCTTTGCCTGCAGCAGCTGGGCAACC 2524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 TGAGGCGGCATCAGCGTACCCACGCAGGCCCCCCACTCCTNCCTGCCGACCTGTGGCT
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                                                                                                         Sequence 1049, Application US/09016434

Sequence 1049, Application US/09016434

Patent No. 650038

GENERAL INFORMATION:
APPLICANT: Jeffrey J. Sellhamer

APPLICANT: Jeffrey J. Sellhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE

CITY: PALO ALIFO

STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 TCGCTGCTGTACTCCACGACCAGCCGGCCTNCCAGTCCCACAGAGCAGGA 235
                             Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PErfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
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92.2%; Pred. No. 6.1e-44;
tive 0; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 94,071
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1049:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
786 CTIGGGCTCATCGACTATCGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.24
Matches 214; Conservative
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CLONE: 999335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-016-434-1049
                                                                                                           US-09-016-434-1049
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                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jenice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
TUBBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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CITY: PALO ALTO
STATE: CALIFORNIA
COUTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: WAS PC-DOS/MS-DOS
SOFTWARE: WORD PETECT 6.1 for Windows/MS-DOS 6.2
CURRENT ARRENT DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
3.0%; Score 113.8; DB 4;
Best Local Similarity 56.6%; Pred. No. 2.1e-19;
Matches 211; Conservative 0; Mismatches 162;
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PILING DATE: HEREWITH
CLASSIFICATION:
PROG APPLICATION DATA:
PAPLICATION UNBER:
FILING DATE:
CLASSIFICATION NUMBER:
ATTONNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCY/AGENT NUMBER: 37,071
REFERENCY/AGENT NUMBER: 37,071
REFERENCY/AGENTON NUMBER: 37,071
RELEPHONE: (650) 855-055
TELECOMMINICATION INFORMATION:
TELECOMMINICATION SEQ ID NO: 1229:
SEQUENCE CHARACTERISTICS:
LENGTH: 2678 BASE DAIES
US-09-016-434-1229
; Sequence 1229, Application US/09016434
; Patent No. 6500938
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2995 CACATGAAGACTCACAGTGGTGAAAACCCTTCCGCTGTGCCCCGCTGTCCATACGCCTCT 3054
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                                                                                                                                                                                                                                                                                             3230 GTATGAACCTCAAACGTCATATGCTGCGACACACGCGAGAAGCCCTTCCGCTGTGCCA 3289
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                                                                     941 Achaericcaecereceneaaaacerrecaecrecrecrecrecrecrecrecrecae 1000
3110 ACAAGTGCCCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAACCTCAAGCGTCATGGTC 3169
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                                                                                                                                                                                                                                                                                                                                                                                                                                        3290 CCTGCGCCTATACCACAGGCCACTGGGACAACTACAAGCGTCATCAGAAGGTGCATGGC 3348
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TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR APPLICATION NUMBER: 09/516,448
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: PARESEQ FOR Windows Version 3.0
SEQ ID NO 427
LENGTH: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 524;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.9%; Score 110.4; DB 4;
5776%; Pred. No. 6.8e-19;
tive 0; Mismatches 146;
                                                                                                                                                  3170 GCATCCACTCTGGTGACAAACCTTTTCGG
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US.49-833-381-427/c
US.49-833-381-427/c
'Sequence 427, Application US/09833381
'Patent No. 6672186
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09418640; Patent No. 6140125; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-427
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US-09-418-640-3
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                                                         761 degadaladectriacaagriccaardaladececaaagecerrcaccricgagecaaccarcere 820
           CCAGAGTATGAACCTCAAACGTCATATGCTGCGACACACGGGCGAGAAGCCCTTCCGCTG 3284
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1058, Application US/09016434
Patent No. 6500338
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCE: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 2416;
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APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION POR SEQ ID NO: 1058:
SEQUENCE CHARACTERISTICS:
LENGTH: Z416 base pairs
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                                                                                                                                                              3285 IGCCACCIGCGCC 3297
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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EDNESS: single
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MEDIUM TYPE: Floppy
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US-09-016-434-1058
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Patent No. 5641672
GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Chaganti, R.S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
TITLE OF INVENTION: ANTISENSE MODULATION OF BCL-6 EXPRESSION
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COUNTRY: United ....
ZIP: 10112
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
^**TWARE: Patentin Release #1.0, Version #1.25
                                    FILE REFERENCE: RTS-0102
CURRENT APPLICATION NUMBER: US/09/418,640
CURRENT FILING DATE: 1999-10-15
CURRENT FILING DATE: 89
SEQ ID NO 3
LENGTH: 3536
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STRENT: 30 Rockefeller Plaza
STRENT: New York
STATE: New York
COUNTRY: United States of America
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CORRESPONDENCE ADDRESS:
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; LOCATION: (328)..(2448)
US-09-418-640-3
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                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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US-08-074-967-1
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2980 AACCACCTGGCTCGGCACATGAAGACTCACAGTGGTGAGAAACCCTTCCGCTGTGCCCGC 3039
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Patent No. 5882858
GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Chaganti, Raju S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDENCE DUINAM LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.6%; Score 100.4; DB 1; Length Best Local Similarity 54.3%; Pred. No. 7.6e-16; Matches 203; Conservative 0; Mismatches 171; Indels
                 NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 0575/43771
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 977-9550
TELEFAX: (212) 64-0525
TELEX: 42223 COOP UI.
SEQUENCE CHARACTERISTICS:
LENGTH: 3720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STREET: 1185 Avenue of the Americas
CITY: New York
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 328..2445
US-08-074-967-1
                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
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US-08-553-541B-1
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APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: CAGAGATLI, Raju S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: May 28, 1996

CLASSIFICATION: 435

ATTONENT APPLICATION: 435

ATTONENT APPLICATION: 435

ATTONENT INPORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US

TELEFRAM: (212) 278-0400

TELEFRAM: (212) 278-0400

TELEFRAM: (212) 391-0525

TELEFRAM: (212) 391-0525

TELEFRAM: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:

LENGTH: 3720 base pairs

TYPE: MUCLAic acid

STRANDEDNES: double
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 54.33
Matches 203; Conservative
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328..2445
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; LOCATION:
US-08-553-541B-1
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GENERAL INFORMATION:
APPLICANT: Dalla-Favera, Riccardo
APPLICANT: Chaganti, R.S.K.
TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
TITLE OF INVENTION: bcl-6
                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/268,202
FILING DATE:
CLASSIFICATION:
ATTORNEY/ACTION:
                                                                                                                                                                                                                                                                                                                                                                              0575/43771-A-PCT-US-Z
                          United States of America
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 391-0525
TELEX: 42523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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328..2445
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New York
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; LOCATION:
US-09-268-202-1
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PCT-US94-06669-1
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                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALIZED FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFTCATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US 08/074,967
FILING DATE: 09-UNW-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 28,678
ERERENENCE/DOCKET NUMBER: 43771-A-PCT
TELECOMMUNICATION INFORMATION:
TELEFONE (212) 977-9550
TELEFAX: (212) 977-9550
TELEFAX: (212) 977-9550
TELEFAX: (212) 977-9550
TELEFAX: (312) 64-0525
TELEFAX: (312) 64-0525
TELEFAX: (312) 64-0525
TELEFAX: (312) 98-0515
TELEFAX: (312) 98-0515
TELEFAX: (312) 98-0515
TELEFAX: 3720 base paire
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                               New York
: United States of America
                                       CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2302 CATTGTGAGAGTG 2315
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LOCATION: 328..2445
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                 CITY: New York
STATE: New Yor
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3104 AGCCCTACAAGTGCCCCCTCTGTCCGTATGCCTGTGGCAACCTGGCCAACCTCAAGCGTC 3163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3044 CATACGCCTCTGCTCATCTGGATAACCTGAAACGGCACCAGCGCGTCCACACAGAGAAA 3103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 2.5%; Score 96.4; DB 4; Length 2769; Best Local Similarity 55.8%; Pred. No. 7.1e-15; Matches 184; Conservative 0; Mismatches 146; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Dohn Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 784CTP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/522,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PF FL Genes Version 1.0
LENGTH: 2769
                   Sequence 309, Application US/09620312D Patent No. 6569662 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: May 14, 2004, 05:50:07 Job time: 266 secs
                                                                                                                                                                                                                               Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
                                                                                                 APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                       Yang, Yonghong
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (248)..(2659)
US-09-620-312D-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
-09-620-312D-309
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NAME/KEY: CDS
LOCATION: (248
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May 13, 2004, 22:44:48 ; Search time 1473 Seconds (without alignments) 11851.918 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                  OM nucleic - nucleic search, using sw model
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2947324 seqs, 2269024515 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-09-673-994A-7 Title: Perfect score: Sequence: Scoring table: Searched:

Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1582, Ap	Sequence 121, App	Sequence 7625, Ap	Seguence 1126, Ap	Sequence 32, Appl	Sequence 32, Appl	Seguence 48, Appl	Seguence 48, Appl	Sequence 48, Appl	Sequence 48, Appl	Sequence 48, Appl	Sequence 7626, Ap	Sequence 636, App	Sequence 1, Appli
QΙ	US-10-108-260A-1582	US-10-221-625-121	US-09-764-891-7625	US-10-094-749-1126	US-10-037-270-32	US-10-117-722-32	US-09-984-245-48	US-09-966-262-48	US-09-983-966-48	US-10-059-395-48	US-10-143-090-48	US-09-764-891-7626	US-09-917-800A-636	US-09-813-319A-1
	16	13	10	16	15	16	σ	10	10	13	15	10	σ	σ
Query Match Length DB	2013	1975	9266	1456	1558	1558	851	851	851	851	851	6271	496	1435
Query Match	39.5	38.9	31.1	29.0	21.2	21.2	13.7	13.7	13.7	13.7	13.7	11.6	10.4	10.0
Score	1518	1498	1195	1115.2	815.2	815.2	528.4	528.4	528.4	528.4		444.8		
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ALIGNMENTS

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                 Sequence 1582, Application US/10108260A

Publication No. US20040005560A1

GENERAL INFORMATION:

APPLICAMT: HELLY RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA

FILE REFREENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOUTHWARE: Patentin Ver. 2.1

SEQ ID NO 1322
                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-10-108-260A-1582
US-10-108-260A-1582
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                                                                                                                                              Query Match
Best Local Similarity 81.3%; Pred. No. 0;
Matches 1568; Conservative 0; Mismatches 216; Indels 144;
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT PILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7625
LENGTH: 9266
                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-7625
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REPERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
PRIOR SECULO BATE: 2001-09-14
NUMBER OF SECULO BATE: 2001-09-14
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                           Sequence 1126, Application US/10094749; Publication No. US20030219741A1; GENERAL INFORMATION:
                                                                                                                                                                                      SUCAL.
OTSUTA, TELEC.
WAKAMATSU, AI
SATO, HIROYUKI
I: ISHII, SHIZUKO
T: YAWAMOTO, JUN-ICHI
                                                                                                                                                                                                                                                                                                              NAGAI, KEIICHI
IRIE, RYOTARO
IRIE, RYOTARO
SEKI, NACHIKO,
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOVUKI
NAGAHARI, KENJI
                                                                                                                                                                     APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
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                           3822 CTAACAGA 3829
                                                       3318 CTAACAAA 3325
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; ORGANISM: Homo sapiens
US-10-094-749-1126
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LENGTH: 1456
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2761 TGTGGAACTGGAACCACTGCCAGAGCTACTGTTCCCTTGGACCTGCCGGGGCTGT
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APPLICANT: Tangy Y. Tom
APPLICANT: Tangy Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219744Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2BGIP
CURRENT APPLICATION NUMBER: US/10/117,722
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Best Local Similarity 85.7%; Pred. No. 1.6e-231;
Matches 1004; Conservative 0; Mismatches 123; Indels 45; Gaps
3778 TITAC----TGTTTTAACTTATTTCAGTGCTTTATAATAAAGGAAACACTAAC 3826
                        APPLICANT: ASHIGI, Vinod
APPLICANT: ASHIGI, Vinod
APPLICANT: AZANG, Jiah
APPLICANT: Ean, Feiyan
APPLICANT: Chan, Rui-hong
APPLICANT: Chan, Rui-hong
APPLICANT: Wehrman, Tom
APPLICANT: Wens, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Mang, Vinothong
APPLICANT: Mang, Dunrui
APPLICANT: Mang, Zhiwei
APPLICANT: Mang, Zhiwei
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APPLICANT: Wang, Lining
APPLICANT: Tillingmat, John
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APPLICANT: Polyeptides
FILE REFERENCE 784CIP2B
FILE REFERENCE 2000-04-25
FRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
FRIOR APPLICATION NUMBER: 09/488,725
FRIOR APPLICATION NUMBER: 09/488,725
FRIOR APPLICATION NUMBER: 09/488,725
FRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: PF_genes Version 1.0
                                                                                                                                 Sequence 32, Application US/10037270; Sequence 32, Application No. US20030104529A1; GENERAL INRORMATION: APPLICANT: Tang, Y. Tom APPLICANT: Liu, Chenghua; APPLICANT: Asundi, Vinod APPLICANT: Chen, Rui, Chen, Rui, APPLICANT: Chen, Rui, Chen, Rui, APPLICANT: Chen, Rui, Chen, Rui, APPLICANT: Chen, Rui, Chen, Rui, APPLICANT: Chen, Rui, Chen, Rui, APPLICANT: Xue, Aidong J. APPLICANT: Xue, Aidong J.
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; NAME/KEY: CDS
; LOCATION: (50)..(1174)
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| Sequence 48, Application US/09984245
| Patent No. US20020165374A1
| GENERAL INFORMATION:
| APPLICANT: Young et al. Application Solution String Prince De Inversion: 87 Human Secreted Proteins TILIE REFERENCE: P2004P1
| CURRENT APPLICATION UNMERR: US/09/984,245
| CURRENT APPLICATION NUMBER: US/09/984,245
| CURRENT APPLICATION NUMBER: US/09/154,707
| PRIOR FILING DATE: 1938-09-17
| PRIOR FILING DATE: 1938-09-17
| PRIOR FILING DATE: 1938-09-17
| PRIOR FILING DATE: 1937-03-21
| PRIOR FILING DATE: 1997-03-21
| PRIOR FILING DATE: 1997-05-30
| PRIOR FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                                                                                                   Score 815.2; DB 16;
Pred. No. 1.6e-231;
0; Mismatches 123;
CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: 09/620,312

PRIOR FILING DATE: 2000-07-19

PRIOR PILING DATE: 2000-07-19

PRIOR PILING DATE: 2000-04-25

PRIOR PILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1104

SEQ ID NO 32

LENGTH: 1558
                                                                                                                                                                                                                                                                                                                                                                   21.2%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 1004; Conservative
                                                                                                                                                                                                                                                                   ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1174)
US-10-117-722-32
                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                           3713 GGCCTTGGATTCACCGCCACTGCTCCCAGAGGCTATGGATGAACTGGTTGGGAG-CTGCC
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TITLE OF INVENTION: 87 Human Secreted Proteins
TITLE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/966,262
CURRENT FILING DATE: 2001-10-01
PRIOR PPLICATION NUMBER: US 09/154,707
PRIOR FILING DATE: 1998-09-17
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PRIOR PELICATION NUMBER: PCT/US98/05311
PRIOR APPLICATION NUMBER: US 60/041,277
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PRIOR PILING DATE: 1997-03-21
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PRIOR APPLICATION NUMBER: US 60/041,281
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83.3%; Pred. No. 3.6e-146;
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NUMBER OF SEQ ID NOS: 343
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Best Local Similarity 83.33
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ORGANISM: Homo sapiens
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Sequence 48, Application US/09983966
; Sequence 48, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; TITLE OF INTENTION: 87 Human Secreted Proteins
; FILE REFRENCE: PZ004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
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                                                                                      Length 851;
                                                                                                                      96; Indels
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                                                                                      Score 528.4; DB 10
Pred. No. 3.6e-146;
0; Mismatches 96;
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US-10-059-395-48
; Sequence 48, Application US/10059395
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Best Local Similarity 83.3%;
Matches 701; Conservative
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-983-966-48
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Pred. No. 3.6e-146;
0; Mismatches 96;
                                                                                                                                                      uvery match 13.7%;
Best Local Similarity 83.3%;
Matches 701; Conservative 0
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver.
SEQ ID NO 48
LENGTH: 851
                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-143-090-48
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                           1 CACATGAAGACACACAGTGGTGAGAAGCCCTTCCGCTGCGCCCGCTGTCCTTATGCCTCT
                                                                                  3055 GCTCATCTGGATAACCTGAAACGGCACCAGCGCGTCCACACAGGAGAAAAGCCCTACAAG
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US-10-143-090-48
; Sequence 48, Application US/10143090
; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et 7. TILE OF INVENITON: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/143,090
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
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Length 851;
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981 ACAAAAGCTAATCGTGCTCATAGTGTCATGCTTTACTCTCCTACCCTGGCCCCATATGTG 1040
CGCTTGCACCCGCTCTCTGTTGTACACTTTTCAAGCAACACTTTTTCAGACTAAAGGCCAA 980
                                                         741 GGCAGCCTGGGAGGCTCTGCTGTCCTTTAAGCCTCCTTACTCTCCTTGGGCTCAŢCGAC
                                                                                                                                                                                                   5837 ACTCTGTGA--ACTTTATTTAAGGACATTCTTTTTTATTGGCGGCTCCATGGCCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                        801 TATCGGTTCTGTGCCTGTGCTCTGTTGTGTTGGAGGGAAGGACTGGTAGTTCTGATTTTT
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                                                                                                          Gaps
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US-09-917-800A-636
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Patent No. US2020119462A1

GENERAL INPORMATION:
APPLICANT: Wendrick, Donna
APPLICANT: Wendrick, Donna
APPLICANT: Castle, Arthur
APPLICANT: Gastle, Arthur
APPLICANT: Gala Logic, Inc.
TILE OF INVENTION: Molecular Toxicology Modeling
FILE REFREENCE: 44921-5038-02
CURRENT APPLICATION NUMBER: US,09/917,800A
CURRENT APPLICATION NUMBER: US,60/222,040
PRIOR APPLICATION NUMBER: US,60/220,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US,60/290,645
PRIOR APPLICATION NUMBER: US,60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US,60/297,457
PRIOR APPLICATION NUMBER: US,60/297,457
PRIOR APPLICATION NUMBER: US,60/297,457
PRIOR APPLICATION NUMBER: US,60/297,457
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PRIOR APPLICATION NUMBER: US,60/297,457
PRIOR APPLICATION NUMBER: US,60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US,60/297,457
PRIOR APPLICATION NUMBER: US,60/297,457
PRIOR APPLICATION NUMBER: US,60/297,457
PRIOR APPLICATION NUMBER: US,60/297,457
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PRIOR APPLICATION NUMBER: US,60/297,457
PRIOR APPLICATION NUMBER: US,60/297,457
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10.4%; Score 399.2; DB 9;
Best Local Similarity 93.0%; Pred. No. 8.5e-108;
Matches 452; Conservative 0; Mismatches 28;
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                                              Sequence 7626, Application US/09764891
; Sequence 7626, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REPRENCE: PC006
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7626
; LENOTH: 6771
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7626
     RESULT 12
US-09-764-891-7626
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APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Lavallie, Edward R.
APPLICANT: Collins.Racie, Lisa A.
APPLICANT: Collins.Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: APPLICANT: Arguell R.
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Relleher, Kerry S.
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
FILE REFERENCE: G1 6000-104
CURRENT FILING DATE: 2002-04-02
BARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 321
SEQ ID NOS: 321
SEQ ID NOS: 321
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US-10-114-893-68
US-10-114-893-68
Sequence 68, Application US/10114893
Publication No. US20020193567A1
GENERAL INFORMATION:
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LOCATION: (24)
10-114-893-68
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FEATURE:
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Sequence 1. Application US/09813319A

Sequence 1. Application US/09813319A

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVE
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                                           GAGGAGGCACTGTCCACGGAGGGGCTGAAGACACCGGCAACAGTGACAAAAAAAGAAGGCC
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                                                                                                                                                          567 AAGAGGGATTAGTGGTCAACCGGACCCTGCCCATGTGGACTGTTTTCTGAGCCCTTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGGCGGCTTTCCTCAGCCCATTCCAAAGAGGC---CTCTCCCTCTGGACGCGCAGC
                                                                          CCGAGACTGAGTTTTGTCCTTGTCCTTTAGCCTTAGCAGTGGGTATGAGGTGTGTGCAGGGG
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Best Local Similarity 85.6%;
Matches 527; Conservative C
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ORGANISM: Human
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JS-09-813-319A-1
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9.8%; Score 376; DB 14; Length 1934; imilarity 82.1%; Pred. No. 1.6e-100; ; Conservative 20; Mismatches 70; Indels 20; Gaps 8;	AGCTGCTGGATCAGTGCCTGGCGCCAGACACTTCTGGGGATGGTACAGGGTGTGACAACA 432	AGCTGCTTGTTCAGTGCCTGGCACCAGACTTTTGGGGATGGTACAGGGTGTGACAACA 1354	TGACGTGCATCATCATTTGTTTCAAGCCCCGAAACACAGTAGAGCTTCAGGCAGAGAGTG 492	rdaccriscarcartracrircaasccccsaaacacascasccasccasasass 1414	GGAAGAGGAACTGGAGGAGCACTGTCCACGAGGGGGCTGAAGACACCGGCAACAGTG 552	gcaagcgaaaactagaggaggtgctctttactgaggggctgaagaaatggcaacagcg 1474	ACAAAAAGAAGGCCAAGAGGGATTAGTGGTCAACCGGA-CCCTGCCCCATGTGGACTG 608	acaagaagaagaggccaaggcgagactagcagtcarccagacccctgcccacytagaytg 1534	TTTTCTGAGCCCT-TGGACCCGAGACTGAGTTTTGTCCTTGTCCTTTAGCCTTAGCAGTG 667	TTTTYTGAGCCTTCCGGACCTGAGAYTGAGTTTTGTYTTTTTCTTTAGCCTTAGCAGTG 1594	GGTATGAGGTGTGCAGGGGGCTGGGTGGCTTTCCTCAGCCCATTACAAAGAGGCCCC 725	GGTATGAGGTGTGCAGGGGGAGCTGGGTTCCAMTCCGCCCATTCCAAAGAGGGTTCT 1654	CCACCCCCCCACGCGGCAGCCTGGGAGGCTCTGCTCCTCTTAAGCCTCCTTCTTC 785	-B	CITGGGCTCAICGACTAICGGTTCTGTGCCTCTGTTGTTGTTTGGAGGGAAGGACTG 845	CTCGGGYTCAICACCGGTTCTGTGTTGTTTGTTGTTGAGGGAAGGACTG 1763	GTAGTICIGATITITACICIGIGAACACITIAITITAAGACAITCITITITATIGGCGGC 905	GCGGTTCTGGTTTTTACTCTGTGAACTTTATTTAAGGACATTYTTTTTTTTGGCGGC 1821	TCTGTGACCCCTAGCGCTTGCACCCGCTCTCTGTTGTACACTTTCAAGCAACACTTTTT 965		CAGACTAAAGGCCAAA 981	CAGACTAAAGGCCAAA 1897	
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Query Match Best Local Sin Matches 506;	373	1295	433	1355	493	1415	553	1475	609	1535	668	1595	726	1655	786	1708	846	1764	906	1822	996	1882	
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Search completed: May 14, 2004, 06:56:11 Job time : 1483 secs Н

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Searched:

Database

Sequence:

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Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D43028M17 product:similar to CDNA FL032203 FIS, CLONE PLACEG003038, WEAKLY SIMILAR TO ZINC FINGER PROTEIN 84 [Homo sapiens], full insert sequence.

AK052459.1 GI:26342688
HTC; CAP FIRMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
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BAW990386
BAW990386
AW536524
AW536524
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CB327866
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BB484959
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Mus musculus (house mouse)
Mus musculus
 RESULT 1
AK052459
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                                              May 13, 2004, 15:34:15 ; Search time 9218 Seconds (without alignments) 12462.552 Million cell updates/sec
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                                                                                                                                                                                 55026578
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                     - nucleic search, using sw model
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Perfect score;
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JOURNAL MEDLINE

AK052459 Mus muscu AL534516 AL534516 BQ749274 UI-M-FD0-BI668143 603295981

AK052459 AL534516 BQ749274 BI668143

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1247 906 735 990

21.5 19.0 18.6 17.9

827.2 732.4 716.2 687.2

Result No.

TITLE

BQ072985 AGENCOURT BQ056860 AGENCOURT BF533491 BX455491 BI408818 602956759 AW990386 uf060503.x BG574616 602596613 AW55624 G0105E04-BM14215 L0801D02-BM14215 L0801D02-BM142850 K0731010-BM245850 K0731010-BM245850 K0731010-BM245850 K0731802-BM19376 603167805 CA450828 UI-M-FV0-BG707470 602672893 C78804 C78804 Mous AM538688 C0110G03-BG352469 G03167805 AW538688 C0110G03-BG55249 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG55240 C0110G03-BG652340 C0110G03-BG65340 C0110G03-BG65340 UI-R-CNI-BC747039 UI-M-CG09 BG77039 UI-M-CG09 BG77039 UI-M-CG09 BG203743 UI-R-ENI-BG203650 UI-R-ENI-BG203650 UI-R-ENI-BG203650 UI-R-ENI-BG20850 UI-R-ENI-BG20850 UI-R-ENI-BG20850 UI-R-ENI-

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HGRIHSGDKPPRCSLCNYSCNQSMNLKRHMLRHTGEKPFRCATCAYTTGHWDNYKRHQ
KVHGHGGAGGPGRSAPPEGWAPPPFPFSVLSTRGPAALGATGSRALHSDSP"
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Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome Exploration Research Group, RIKEN Gordences Center (GSC), Exploration Research Group, RIKEN Gordences Center (GSC), Kanagawa 230-0045, Japan (E-mail:genome-res@ggsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kabiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Warahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Murameteu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format General Res. 10 (11), 1757-1771 (2000)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev_stage="13 days embryo"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (Dases I to 1247)
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similar to CDNA FLJ32203 FIS, CLONE PLACE6003038, WEAKLY
SIMILAR TO ZINC FINGER PROTEIN 84 [Homo sapiens]
(SPTM 1956Mi3, evidence: FASTY, 75.2%ID, 58.9%length,
match=666)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase II Team and the
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
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/mol_type="mRNA"
/strain="C57BL/63"
/db_xref="FaNTOM DB:D430028M17"
/db_xref="MG1:2421883"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Bammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 735)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Enail: cgapba-rafmailinh.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Parayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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BQ749274 GI:21896061
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Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 906)

Li,Wab. Gruber.C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Li mpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12798009.

Contact: Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Invitrogen. This sequence belongs to sequence cluster 1341.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODF004BB06QPIkcluster=1341.r. Contact : Feng Liang Email: fliang@lifetech.com URL:

Faraday Avenue Genoscope sequence ID : CSODF004BB06QPI.

Location/Qualifiers
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                                                   1079 ATAGACCAGGGGACTIGICTTAGCTCACGTACCAGAIGAGCTAAGTGATTAGGGCCTTGG
                                                                                                                                    3721 ATTCACCGCCACTGCTCCCACAGGCTATGGATGAACTGGTTGGGAGCTGCCCAGCCTTT
ATAGACCAGGGGACTTGTCTTAGCTCACGTACCAGATGAGCTAAGTGATTAGGGCCTTGG
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1 (Dases; 1 to 990)

2 NIH-MGC http://mgc.nci.nih.gov/,
National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

2 Contact: Robert Strausberg, Ph.D.

2 Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

2 Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Miklos Palkovits, M.D., Contact
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603295981F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5314868 5',
                                                                                                                                                                                                                                   2352 CCACCTGAAGCGGCACATGCAGACACACAGGGGGGAGAAGCCGTTCCGCTGTGGGCGCTG
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                                                          3497 AGGTTCTTTTACCTGGGGCTCTAGGAATTAGCCCTATGCCTCCTGCATTTATACAAATG
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85.6%; Pred. No. 7.7e-105;
tive 0; Mismatches 129; Indels 13;
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Best Local Similarity 99.2%; Pred. No. 1.2e-109;
Matches 729; Conservative 0; Mismatches 5;
                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                      "mol_type="mRNA"
|strain="C57BL/6"
|db_xref="taxon:10090"
                        Seq primer: pXX-5.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3257
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 1669)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity 92.1
735; Conservative
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Best Local Si
Matches 735,
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BQ072985
BQ072985.1 GI:19902031
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2952 ITTATGCCCCTTTGCCACTCACTACCCCCAACCACCTCGGCACATGAAGACTCACAG
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                                                                        GAAGCCCTACCGTTGTCCCCACTGCCCTTTGCCTGCAGCCTGGGGCAACCTGAAGGCG
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/lab_host="DH10B (phage-resistant)"
/lab_host="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
inco ECORI/XhoI sites using the following s' adaptor:
GCCACAAG(G). Size-selected -500bp for average insert size
1: 8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Pred. No. 1.5e-102;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5809303"
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.
1 '(Dasses 1 to 843)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                     CGCCTCTGCTCATCTGGATAACCTGAAACGGCACCAGGGGGTCCACACAGAGAAAAGCC 3107
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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 929)
1 (bases 1 to 929)
1 (Aruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY Cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
library was constructed by life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1341.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAI009ZF12 CSOO862 Z&cluster=1341.r.
Contact : Feng Liang Email : fliang@llfetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID : CSOBAI009ZF12_CSOO862_2.
Location/Qualifiers
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                                                                    2988 GGCTCGGCACATGAAGACTCACAGTGGTGAGAAACCCTTCCGCTGTGCCCGCTGTCCATA
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Contact: Robert Straubberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDDA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Conscrtium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Conscrtium/LLNL at:
http://mage.lln.gov
Plate: LLAM9782 row: 1 column: 06
High quality sequence stop: 817.
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                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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Mus musculus
Mus musculus
Mus musculus
Muscazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mumania; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 646)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Ontational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/Organizes Thus missenins / Organizes | Molitype="mRNA" | Molitype="mRNA" | Molitype="mRNA" | Molitype="mRNA" | Molitype="mRNA" | Molitype="pooled lung tumors" | Alab.host="MINGS | Molitype="pooled lung tumors" | Alab.host="MINGS (Phage-resistant) | Alab.host="MINGS (Phage-resistant) | Alab.host="molitype | Molitype |
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                                                                                                                                           CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NGI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11295 row: j column: 18
High quality sequence start: 7
High quality sequence stop: 646.
High quality sequence stop: 646.
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Email: cgapbs-r@mail.nih.gov
Tiseue Procurement: Gilbert Smith, Ph.D.
DDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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16.3%; Score 628; DB 12; Length 646;
Best Local Similarity 99.8%; Pred. No. 7e-95;
Matches 639; Conservative 0; Mismatches 0; Indels
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3666 CCAGGGGACTIGICITAGCTCACGTACCAGATGAGCTAAGTGATTAGGGCCTTGGATTCA 3725
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I. (bases 1 to 694)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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(Dipublished-(1997)
(Cher ESTS: uf06c03.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is avallable royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:937416
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16.2%, Score 623.6; DB 10; Length 694;
Best Local Similarity 94.8%; Pred. No. 3.7e-94;
Matches 655; Conservative 0; Mismatches 35; Indels 1; Gaps
                                                                                                              3726 CCGCCACTGCTCCCAGAGGCTATGGATGAACTGGTTGGGA 3765
                                                                                                                                                CCGCCACTGCTCCCAGAGGCTATGGATGAACTGGTTGGGA 8
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/tissue_type="mammary gland"
/lab_host="DH108"
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:1510564"
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BG574616 193 bp mRNA linear MESTS10EAPRS2001.0 602596613F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4705610 5',
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
Tissue Procurement: DCTD/DTP
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM10572 row: i column: 03
High quality sequence stop: 750.
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                                                        451 gececreadeenredececeaerrearaceceaecrererrandaeaeredesereea 392
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1. (bases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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/tissue_type="mismo y adenocarcinoma, cell line"
/lab.host="DHIOB (phage-resistant)"
/clone_lib="NIH MGC 87"
/note="Cram: breast; Vector: pCMV-SPORT6; Site_l: Notl;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
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3379 GCCCCTGAGGCCTGGGCCCCACCTCATAGCCCACCCTCTGTTTGAGCCACTCGAGGGTCCA
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Homo sapiens
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cocation/Qualifiers
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 full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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                                                       16:0%; Score 616.2; DB 12; Length ilarity 89:9%; Pred. No. 6e-93; Conservative 0; Mismatches 74; Indels
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AW536524.1 GI:7178941
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/lab host="DH108"
/clone lib="DH108"
/clone lib="NH Mouse E7.5 Embryonic Portion cDNA Library"
/note="Vector: pSPORT1 (Gibco/BRL Life Technology);
/ste 1: Sal1; Site 2: Not1; Total RNAs were extracted from 5 Embryo. The double-stranded cDNA was synthesized by gibco's kit with an Oligo(dI) primer [NotI primer-adapter
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases I to 628)

Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genner-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
Proc: Natl Nacad: Sci. U.S.A. 97 (16): 9127-9132 (2000)
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
ational Institute on Aging/National Institutes of Health
Email: Casell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: G1015 row: E column: 04
Seg primer: -21M13 Forward
High quality sequence stop: 628
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16.0%; Score 613.8; DB 10; Length
Best Local Similarity #999.7%; Pred. No. 1.7e-92;
Matches 615; Conservative 0; Mismatches 2; Indels
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/mol_type="Mus musculus"
/mol_type="MuskNa"
/strain="C57BL/64"
/db_xref="niaEST:G0105E04-3"
/db_xref="caxon:10090"
/clone="G0105E04"
/sex="unknown"
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AW536842 AW536842.1 GI:7179259
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Wood,W.H. III, Becker,K.G. and Ko,M.S.H.

embryo using a 15,000 mouse developmental cDNA microarray
arccc.,Matl.e.Acad.e.Sci.e.U.S.A...9728(16)?**9127-91328(2000)
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                                                         CTGAGCCCTTGGACCCGAGACTGAGTTTTGTCCTTGTCCTTTAGCCTTAGCAGTGGGTAT
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 ACAAAAAGGCCAAGAGGGATTAGTGGTCAACCGGACCCTGCCCATGTGGACTGTTTT
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Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: G0109 row: D column: 12
Seq primer: -21M13 Forward
High quality sequence stop: 666
POLYA-Yes.
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/mol_type="mRNA"
/strain="C5TBL/G"
/db_xref="miaEST:G0109D12-3"
/db_xref="taxon:10090"
/clone="G0109D12"
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MEDLINE
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AUTHORS
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[5-pgAcracarcocgaccgcccccrrrrrrrrrrrrrrrr] [from 0.51ug of mRNA . The double-stranded cDNAs were treated with T4 DNA polymerase and purified by ethanol-precipitation. The cDNAs were ligated to cone-linker LL-Sal3 (include Sal1 sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Tag polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centricon 100. The CDNAs were digested with Sal1 and NotI enzymes. Then, the CDNAs were closed by Gibco's Size Fractionation Column. The cDNAs were closed into Sal1/NotI site of pSDORTH plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang and Minoru S. H. Ko. "
/clone lib="NITA Mouse E7.5 Embryonic Portion cDNA Library"
/note="Vector: pSPORTI (Gibco/BRL Life Technology);
Site 1: Sall; Site 2: NotI; Total RNAs were extracted from 6 Embryo. The double-stranded cDNA was synthesized by Gibco's kit with an Oligo(dT) primer [NotI primer-adapter from GibcoBRL]
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258 792 912

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Mus musculus Eukaryota, Atazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Maranalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 727)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM119847
L0931C10-3 NIA Mouse Newborn Kidney cDNA Library (Long) Mus musulus cDNA clone NIA:L0931C10 IMAGE:30003009 3', mRNA sequence.
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497 GCAAGAGGAAACTGGAGGAAGGCACTGTCCACGGAGGGGGCTGAAGACACCGGCAACAGTG
                                                                                                     437 ACAAAAAGAAGGCCAAGAGGGACTAGTGGTCAACCGGACCCTGCCCATGTGGACTGTTTT
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                                                            553 ACAAAAAGAAGGCCAAGAGGGATTAGTGGTCAACCGGACCCTGCCCATGTGGACTGTTTT
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On Nov 26, 2001 this sequence version replaced gi:17087873.
Contact: Dawood B. Dudekula
Laboraatc: Dawood B. Dudekula
National Institute on Aging/National Institutes of Health
33 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0931 row: C column: 10
Seq primer: -21M13 Forward
High quality sequence stop: 727
POLYA-Yes.
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                                                                                         BMI14215 10801D02-3 NIA Mouse Newborn Brain cDNA Library Mus musculus CDNA COORE LO801D02 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (Dases 1 to 692)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Pantano,S., Lim,M.K. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 AGCTGCTGGATCAGTGCCTGGCGCCAGACACTTCTGGGGATGGTACAGGGTGTGACAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contract: Dawood B. Dudekula
Contract: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
33 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdnaelgsun.grc.nia.nih.gov
Plate: LOB01 row: D column: 02
Seg primer: -21M13 Forward
High quality sequence stop: 692
POLYA=Yes.
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16.0%; Score 613.8; DB 12; Length
Best Local Similarity 99.7%; Pred. No. 1.6e-92;
Matches 615; Conservative 0; Mismatches 2; Indels
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Site=1: Sal1; Site=2: Not: Mouse cDNA project by the
Laboratory of Genefics, National Institute on Aging (NIA);
Intramural Research Program, NIH
(http://Jgsun.grc.nia.nih.gov/cDNA). This is a
long-transcript enriched cDNA library (Ref. Genome Res.
11:153-1558 (2001). [PMID:11544199]). In
brief,double-stranded CDNA were synthesized with an
Oligo(dT) primer [Invitrogen: 5'pgACTAGTTCTAGARCGCGAGCGCCCTTTTTTTTTTTTTT-1'] from 26
microgram of total RNA, treated with T4 DNA polymerase,
and purified by ethanol-precipitation. The cDNAs were
ligated to Lone-linker LL-Sal4, purified by
phenol/chloroform, and separated from free linkers by
Centricon 100. Then, the cDNAs were amplified by
long-range high fidelity PCR using Ex Taq polymerase
(Takara) with a primer Sal4-S. The products were purified
by phenol/chloroform and Centricon 100. The cDNAs were
digested with Sal1 and Not1 enzymes, and cloned into
Sal1/Not1 site of pSPORT1 plasmid vector. The DH10B E
coli host was transformed with ligation mixture by the
standard chemical method. The average insert size is about
3.0 kb. The library was constructed by Yulan Piao (NIA)."

Query Match
16.0%; Score 613.8; DB 12; Length 727;
Best Local Similarity 99.7%; Pred. No. 1.6e-92;
Matches 615; Conservative 0; Mismatches 2; Indels 0; Gaps 0

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673 GAGGTGGAGGGGGTTTTCGTCCTTGTCCTTTAGCCTTAGCAGTGGGTAT 3.18
117 GAGGTGGAGGGGGTTTTCCTCGTCGCCATTACAAAGAGGGCCCCCCACCC 732
117 GAGGTGGAGGGGCTGGGGGTTTCCTCGTCATTACAAAGAGGGCCCCCACCC 2.58
118 GAGGTGGAGGGGTTTCCTCAGCCCATTACAAAGAGGGCCCCCACCC 2.58
119 GAGGTGGAGGGGTTTCCTCAGCCCTTACAAAGAGGGCCCCCACCC 2.58

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Search completed: May 14, 2004, 05:45:48 Job time : 9239 secs